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GenCore version 5.1.6
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- protein search, using sw model OM protein August 30, 2004, 17:00:32; Search time 38 Seconds (without alignments) 192.383 Million cell updates/sec Run on:

07330446.PEP 405 1 gpdainapvtccynftnrki.....qkwvqdsmdhldkgtgtpkt Title: Perfect score: Sequence:

16

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
5: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	monocyte chemoattr	monocyte chemotact	monocyte chemotact	eotaxin precursor	monocyte chemotact		PDGF-inducible JE	immediate-early se	monocyte chemoattr	eotaxin precursor	eotaxin precursor	monocytic cytokine	LD78-beta protein	macrophage inflamm	macrophage inflamm					monocyte chemoattr	lymphocyte and mon	monocyte chemoattr	I-309 protein prec	lymphotactin precu	monocyte adherence				
n																														
i Y	-	! !						•				•																		
SUMMAKIS	ID	A60299	JC2136	A39296	m	146857	A55984	A54678	JC4912	JC5295	JC2417	A30209	S07723	I48147	I48099	JC2478	A48093	B35673	A30574	A31767	I46730	C30552	I52322	A32393	A46539	JE0177	A28815	A37236	ETHUL	C60407
	DB	7	0	H	~		7			~	Ŋ	Н	н	N	(7)	~	~	~	~	-	~	7	7	7	Н,	~	Н	~	Н	N
	Length	66	9	99	99	125	72	109	97	66	66	148	148	120	96	96	97	93	92	92	92	92	92	92	91	120	91	96	114	20
ф	Query	100.0	83.2	77.8	77.8	77.5	71.1	70.9	66.7	66.2			59.5	58.3	52.8	51.1	49.4	35.9		33.5	33.0	31.5	30.4	29.4	26.8	Θ	26.0	24.6	24.6	24.2
	Score	405	337	315	315	314	288	287	270	268	261	252	241	236	214	207	200	145.5	142.5	135.5	133.5	127.5	123	119	108.5	106	105.5	99.5	99.5	8
	Result No.	н	71	ო	4	S	9	. 7	Φ	σ	10	11	12	13	14	15	16	17	18	64	20	21	22	23	24	25	26	27	28	29

interleukin-8 prec	.TCA3 protein - mou	lymphotactin precu	Neutrophil attract	interleukin-8 prec	interleukin-8 - ra	interleukin-8 - do	gene C10 protein -	interleukin-8 prec	cellobiose-phospho	hypothetical prote	F54F2.8 protein -	hypothetical prote		_	hypothetical prote
A53096	S24236	ETMSL	I48148	342496	146871	JN0841	149555	A37034	AG3481	\$76162	S44825	T26700	E90097	F96831	AB2020
7	7	- -4	7	~	7	7	7	(7)	7	7	~1	7	7	7	7
103	92	114	101	101	101	9	116	9	2867	143	282	363	1019	1076	853
23.2	23.1	22.6	20.5	19.5	19.5	18.5	18.1	17.3	16.3	16.2	16.0	15.9	15.8	15.8	15.4
94	93.5	91.5	83	79	79	75	73.5	70	99	65.5	65	64.5	64	64	62.5
30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	4.5

ALIGNMENTS

RESULT 1				
A60299				
monogyte	monocyte chemoattractant	protein	predursor -	- human

N;Alternate names: GDCF-1; glioma-derived monocyte chemotactic factor 1; MCAF; MCP-1; monocyte chemotactic factor 2 (GDCF-2)
C;Species: Home saptens (man)
C;Dates: Home saptens (man)
C;Dates: 20-Feb-1993 #sequence revision 20-Feb-1993 #text change 16-Jul-1999
C;Accession: A35474; A33476; S03339; IS1841; A60299; A32300; A32396; A34561; IS7488; JCI!
R;Shyy, Y.J.; Li, Y.S.; Kolattukudy, P.E.
Biochem. Biophys. Res. Commun. 169, 346-151, 1990
A;Title: Structure of human monocyte chemotacter protein gene and its regulation by TPA. A;Reference number: A35474; MUID:90290466; PMID:2357211

A; Molecule type: DNA
A; Residues: 1-99 csH7.
A; Residues: 1-99 csH7.
A; Cross-references: GB:M37719; NID:g187447; PIDN:AA18102.1; PID:g487124
A; Cross-references: GB:M37719; NID:g187447; PIDN:AA18102.1; PID:g487124
B; Rollins, B.J.; Stier, P.; Ernset, F; Mong, G.G.
Mol. Cell. Biol. 9, 4687-4695 (1989)
A; A; Title: The human homolog of %the PE gene encodes a monocyte secretory protein.
A; Reference number: A33476; MUID:90097880; PMID:2513477
A; Accession: A33476
A; Molecule type: mRNA
A; Residues: 1-99 cROL>

A;Cross-references: GB:N30816; GB:N31625; GB:N31626; NID:g188701; FIDN:AA36330.1; FID:g X;Voshimuxa, T.;Yubki, N.; Moore, S.K.; Appella, B.; Lerman, M.I.; Leonard, E.J. FEBS Lett. 244, 487-493 (1989) A;Title: Human monocyte chameetractant protein-1 (MCP-1). Full-length cDNA cloning, exp

A;Reference number: S03339; MUID:89153605; PMID:2465924 A;Accession: S03339 A;Status: not compared with conceptual translation

A; Molecule type: mRNA
A; Residues: 1-99 < YOS>
A; Residues: 1-99 < YOS>
A; Cross-references: GB:X14768; NID:g34513; PIDN:CAA32876.1; PID:g34514
A; Cross-references: GB:X14768; NID:g34513; PIDN:CAA32876.1; PID:g34514
A; Experimental source: glioma cell line U-105MG
R; Yoshimura, T.; Leonard, E.J.
R; Yoshimura, T.; Leonard, E.J.
A; Yoshimura, T.; Leonard, E.J.
A; Reference number: 151841; MUID:92095166; PMID:1661560
A; Reference number: MUID:92095166; PMID:1661560

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-99 <YO2>
A;Across-references: GB:S71513; NID:g240867; PIDN:AAB20651.1; PID:g240868
R;Bottazzi, B.; Colotta, F.;Sica, A.; Nobili, N.; Mantovani, A.
Int. J. Cancer 45, 795-797, (1990)
A;Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic f

A; Reference number: A60299; MUID: 90216082; PMID: 2182547

A; Accession: A60299

A;Status: not compared with conceptual translation A;Molecule type: mRNA

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A;Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Analysi A;Reference number: JC2136; MUID:94183284; PMID:7510962
A;Accession: JC2136
A;Accession: JC2136
A;Residues: 1-99 <HOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monocyte chemoattractant protein 1 precursor - bovine
NyAlternate names: monocyte chemotactic factor 1; seminal plasma protein P6
C;Species: Bos primiganius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A39296; B39296
C;Accession: A39296; B39296; MUDD:92096117; PMID:1721821
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A;Residues: 1-99 - vWEM>
A;Cross-references: GB:M84602; GB:M85264; NID:g163394; PIDN:AAA30651.1; PID:g163395
A;Accession: B39296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-99 <2AC>
A;Cross-references: EMBL:X79416; NID:9872312; PIDN:CAAS5945.1; PID:9872313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 QPDAINSPVTCCYTLISKKISMQRLMSYRRVISSKCPKEAVIFKTIAGKEICAEPKQKWV
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                                                                                                                                                          A;Cross-references: GB:Z48479; NID:g683716; PIDN:CAA88370.1; PID:g683717
R;Zach, O.
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83.2%; Score 337; DB 2; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.6e-31;
Matches 60; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
77.8%; Score 315; DB 1; Length 99;
Best Local Similarity 73.3%; Pred. No. 5.3e-29;
Matches 55; Conservative 13; Mismatches 7; Indels
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F;1-23/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: ġlycoprotein
F;1-23/Domain: signal sequence #status predicted
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A,Reaidues: 50-68,'X',70-74,'X',76 <WE2>
A,Experiment 50-68,'X',70-74,'X',76 <WE2>
C,Superfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Superfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, July 1994
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84 QDSINYLNKKNQTPK 98
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                                                                                                                                                                                                                                                                                                   A; Reference number: S57497
A; Accession: S57498
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JC2336
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           A; Residues: 1-99 < EDOT>

A; Residues: 1-99 < EDOT>

B; Furutani, Y:; Nomura, H:; Notake, M:; Oyamada, Y:; Fukui, T.; Yamada, M.; Larsen, C.G. B; Diochem.

Biochem. Biophys. Res. Commun. 159, 249-255, 1989

A; Fitle: Cloning and sequencing of the cDN5, 1989

A; Reference number: A32300; MUID:89165862; PMID:2923622

A; Accession: A32300

A; Residues: not compared with conceptual translation

A; Molecule type: mRNA

A; Residues: Tog ergr.

A; Residues: Tog ergr.

B; Robinson, E.A; Yoshimura, T.; Leonard, E.J; Tanaka, S.; Griffin, P.R.; Shabanowitz, Proc. Natl. Acad. Sci. U.S.A. 86, 1850-1884, 1989

A; Residues: A32396; MUID:89184525; PMID:2648385

A; Molecule type: protein

A; Residues: YX, 25-99 < ROB>

R; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.

B; Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.
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A;Molecule type: protein
A;Residues: 29-33,'XX',36-52,82-92 <DEC>
R;Li, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E.
R»D. Cell. Blochem: 126, 61-68, 1993
A;Title: The expression of monocyte chemotactic protein (MCP-1) in human vascular endoth
A;Reference number: 157488; MUID:94150478; PMID:8107690
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-99 < LIY>
A;Cross-references: GB:869738; NID:g545464; PIDN:AAB29926.1; PID:g545465
A;Cross-references: GB:869738; NID:g545464; PIDN:AAB29926.1; PID:g545465
A;Cross-references: GB:869738; NID:g545464; PIDN:AAB29926.1; PID:g545465
A;Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.
A;Title: The PCR, cloning and sequencing of human monocyte chemoattractant protein-1
A;Reference number: JC1096
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monocyte chemoattractant domesrica (domesric pig)
c;Speis: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999
C;Accession: JC2136; S57498
R;Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994
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A,Molecule type: mRNA
A,Residues: 24-28,'Q',30-99 <YEQ>
C,Genetics:
A,Gene: GDB:SCYA2
A,Cross-references: GDB:125279; OMIM:158105
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C; Superfamily: macrophage inflammatory protein

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C;Accession: A54679; J01478; S32222
R;Opdenakker, G; Fiten, P.; Nys, G; Froyen, G; Van Roy, N.; Speleman, F.; Laureys, G.
R;Opdenakker, G; Fiten, P.; Nys, G; Froyen, G; Van Roy, N.; Speleman, F.; Laureys, G.
A;Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the A;Reference number: A54678; MUID:94375065; PMID:7916328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A54678
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-109 <-ODD>
A;Cross-references: GB:X72309
R;Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
A;Cross-references: Res. Commun. 191, 535-542, 1993
A;Title: Human moncyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and A;Reference number: JC1478; MUID:93213290; PMID:8461011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:X72308; GB:857464; NID:g3928270; PIDN:CAA51055.1; PID:g313708
R;Minty, A.; Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux, submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattrac A;Reference number: S32222
A;Accession: S32222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)resavers: 1-12 viii.
A)resavers: 1-12 viii.
A)resavers: 1-12 viii.
A)ross-references: EMBL:X71087; NID:g288395; PIDN:CAA50405.1; PID:g288397
C; Comment: This protein induces proteinase secretion and chemotaxis by macrophages and rocas cannot seem to the protein induces proteinase secretion and chemotaxis by macrophages and rocas a) Genetics:
A; Genetics: GDS:138473; OMIM:158106
A; Cross-references: GDB:138473; OMIM:158106
A; Introns: 36/1; 75/2
C; Superfamily: macrophage inflammatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OPDAINAPVICCYNFINRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
                                                                                                                                                                                         1 DAINSPYTCCYTLTSKKISMQRLMSYRRVTSSKCPKBAVIFKTIAGKEIXAEP--KWVQD
                                                                                                                                                         3 DAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKIIVAKEICADPKQKWVQD
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C; Keywords: cytokine; glycoprotein; inflammation
Fp. 133/Domain: signal sequence #status predicted <SIG>
F; 34-109/Product: monocyte chemotactic protein 3 #status predicted
F; 39/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 9.6e-26;
4; Mismatches 17; Indels
                                                Length 72;
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                            ; DB 2; Lem.
. 4.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         monocyte chemotactic protein 3 precursor - human
                                                      Score 288; DB
Pred. No. 4.9e
8; Mismatches
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1 Similarity 72.0%; Pre
54; Conservative 4;
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74.08;
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                                                                            Local Similarity 74.0 hes 54; Conservative
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A;Residues: 1-109 <0P2>
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A; Residues: 1-109 <MIN>
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Best Local Similarity
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C;Species: Bos primigenius taurus (cattle)
C;Daccies: Bos primigenius taurus (cattle)
C;Daccession: A55984
R;Procest, P.; Wuyts, A.; Lenaerts, J.P.; Van Damme, J.
Biochemistry 33, 13406-13412, 1994
A;Title: Purification, sequence analysis, and biological characterization of a second la Reference number: A55984
A;Reference number: A55984
A;Reference number: A55984
A;Molecule type: protein
A;Residues: 1-72 <PRO>
monocyte chemoattractant protein-1 - bovine
C;Species: Bos prinigenius indicus (zebu cattle)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-May-1996
C;Accession: UC2336
B;Wempe, F:; Kuhlmann, U.K.; Scheit, K.H.
B;Wempe, F:; Kuhlmann, U.K.; Scheit, K.H.
A;Title: Characterization of the bovine monocyte chemoattractant protein-i gene.
A;Reference number: UC2336; MUID:94338337; PMID:8060303
A;Accession: UC2336
A;Molecule type: protein
A;Residues: 1-99 <WEM>
C;Genetics:
A;Genetics:
A;Genee: MCP-1
A;Introns: 26/1; 65/2
C;Superfamily: macrophage inflammatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 99;
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Best Local Similarity 73.3%; Pred. No. 5.3e-29;
Matches 55; Conservative 13; Mismatches 7; Indels
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Best Local Similarity 75.0%; Pred. No. 8.8e-29;
Matches 57; Conservative 10; Mismatches 9;
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QDAIANLDKKMQTPKT 99
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C; Accession: JC2417
R; Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
R; Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
B; Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
B; Hosang, K.; Knoke, I.; Kes. Commun. 205, 148-153, 199
A; Reference number: JC2417; MUD:95091716; PMID:7999015
A; Accession: JC2417
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: I-99 < HOS.
A; Access-references: GB:248480; NID:9683718; PIDN:CAA88371.1; PID:9683719
A; Experimental source: Corpus luteum
C; Superfamily: macrophage inflammatory protein
C; Superfamily: macrophage inflammatory protein
F; 1-23/Domain: signal sequence #status predicted <NAT>
F; 24-99/Product: monocyte chemoattractant protein-2 #status predicted <NAT>
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cibate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CiAccession: A30209; A44771; A30861
R;Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
R;Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
A;Title: Cloning and expression of JE, a gene inducible by platelet-derived growth factor
A;Reference number: A30209; MUID:88234501; PMID:3287374
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A;Cross-references: GB:M19681; NID:g193486; PIDN:AAA37684.1; PID:g387168; GB:M19682
R;Kawahara, R.S.; Deuel, T.F.
B;Kawahara, R.S.; Deuel, T.F.
J. Biol. Chem. 264, 679-682, 1989
A;Title: Platelet-derived growth factor-inducible gene JE is a member of a family of A;Reference number: A44771; MUID:89093129; PMID:2910858
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           24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 16-Jul-1999
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C.Genetics:
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C;Keywords: cytokine; glycoprotein
F;126/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.4%; Score 261; DB 2; Length 99; 60.0%; Pred. No. 8.3e-23; ive 16; Mismatches 14; Indels
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A; Residues: 1-148 < KA2>
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Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A30209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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ectaxin precursor - human
C; Species; Homo saptens (man)
C; Species; Homo saptens (man)
C; Species; Homo saptens (man)
C; Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
C; Accession: 074912
R; Bartels, J; Schlueter, C.; Richter, E; Noso, N.; Kulke, R.; Christophers, E.; Schroe Biochem. Biophys. Res Commun. 225, 1045-1051, 1996
A; Title: Human dermal fibroblasts sorperss ectaxin: Molecular cloning, mRNA expression, 64; Title: Human dermal fibroblasts sorpers sorpers; C4912; MUD:96374440; PMID:8780731
A; Reference number: JC4912; MUD:96374440; PMID:8780731
A; Reference number: JC4912; MUD:91531982; PIDN:CAA99997.1; PID:g1531983
A; References: EMBL:275668; NID:g1531982; PIDN:CAA99997.1; PID:g1531983
A; References: EMBL:275668; NID:g1531982; PIDN:CAA99997.1; PID:g1531983
A; Reference manner: This protein has eosinophil specific chemotatic activity.
C; Commentumin source: dermal fibroblast
C; Commentumin: signal sequence #status predicted <NIT>
F; 1-18/Domain: signal sequence #status predicted <NIT>
F; 19-97/Product: eotaxin #status predicted <NIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A MOLECULE type: mRNA
A;Residues: 1-99 < vAN>
A;Residues: 1-99 < vAN>
A;Residues: 1-99 < vAN>
A;Cross-references: GB:Y10802; NID:g1924937; PIDN:CAA71760.1; PID:g1924938
A;Experimental source: bone marrow
C;Comment: This protein belongs to the beta-chemokine family which is one of the major H
tis and in tumor biology, and contribute to the trafficking and recuitment of the respon
C;Genetics:
C;Superfamily: macrophage inflammatory protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemotactic protein-2 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monocyte chemotactic protein-2 precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: O2-May-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000
C;Accession: JG5295
R;Van Coillie, E.; Froyen, G.; Nomiyama, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van Da Biochem. Biophys. Res. Commun. 31, 726-730, 1997
A;Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression of A;Reference number: JG5295; MUID:97224420; PMID:9070881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 NAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKIIVAKEICADPKQKWVQDSMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 97;
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Pred. No. 7.6e-24;
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JC2417
monocyte chemoattractant protein-2 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
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66.7%;

Conservative

Best Local Similarity Matches 47; Conserv

Query Match

66 НЕВКОТОТРК 75 YLDOKSPTPK 96

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g 8

RESULT 9 JC5295

Sma.

immediate-early serum-responsive protein JE precursor - rat

47; Conservative

Matches

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Query Match Best Local Similarity

A; Accession: JC5295

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 16-Jul-1999
C;Accession: JC2478
R;Jose, P.J.; Adcock, I.M.; Griffiths-Johnson, D.A.; Berkman, N.; Wells, T.N.C.; William Biochem. Biophys. Res. Commun. 205, 788-794, 1994
A;Title: Botaxin: Cloning of an eosinophil chemoattractant cytokine and increased mRNA e
                                                                                                                                                                                              C. incleasion: 130033

R. Rochenberg, M.E.; Luster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.

J. Exp. Med. 181, 1211-1216, 1995

A; Title: Constitutive and allergen-induced expression of ectaxin mRNA in the guinea pig
A; Reference number: 148099; MUID:95173589; PMID:7869037

A; Recession: 148099

A; Status: preliminary; translated from GB/EMBL/DDEJ

A; Molecule type: mRNA

A; Residues: 1-96 < RES

A; Cross-references: EMBL:U18941; NID:9687655; PIDN:AAC52180.1; PID:96687656

C; Superfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 PVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKBICADPKQKWVQDSMDHL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 PSACCFRVINKKISFQRLKSYKIIISSKCPQTAIVFEIKPDKMICADPKKKWVQDAKKYL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A;Residues: 1-96 <10S>
A;Cross-references: EMBL:X77603; NID:g602551; PIDN:CAA54698.1; PID:g602552
C;Comment: This protein is identified as a potent eosinophil chemoattractant.
C;Superfamily: macrophage inflammatory protein
                                                           eotaxin precursor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: 148099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.8%; Score 214; DB 2; ilarity 57.4%; Pred. No. 2e-17; Conservative 12; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: August 30, 2004, 17:08:02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 GQISÕTTK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 DQISQTTK 95
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Best Local Similarity
Matches 39; Conserv
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N; Alternate names: monocyte chemoattractant protein-1
C; Species: Rattus norregious (Norway rat)
C; Species: Rattus norregious (Norway rat)
C; Date: 10.58p-1999 #sequence_revision 10.58p-1999 #text_change 10.58p-1999
C; Accession: S0723; JN0128
R; Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res: 18 23-34, 1990
A; Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential
A; Reference number: S07723; MUID: 90174947; PMID: 2106664
A; Residues: 1-148 ATM
A; Residues: 144 ATM
A; Residues
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R;Yoshimura, T.
J. Immunol. 150, 5025-5032, 1993
A;Title: cDNA, cloning of guinea pig monocyte chemoattractant protein-1 and expression A;Reference number: I48147; MUID:93267104; PMID:8496603
A;Accession: I48147
A;Status: preliminary; translated from GB/BMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monocyte chemoattractant protein-1 - guinea pig
C,Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #seguence_revision 02-Jul-1996 #text_change 16-Jul-1999
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A; Residues: 1-120 <RES>
A; Cross=references: GB:L04985; NID:g349820; PIDN:AAA37047.1; PID:g349821
C; Genetics:
A; Genetics:
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Best Local Similarity 59.7%; Pred. No. 7.4e-20;
Matches 43; Conservative 14; Mismatches 13; Indels
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Best Local Similarity 100.0%; Pred. No. 6.1e-47; Matches 76; Conservative 0; Mismatches 0;
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Sequence 5, Appli
Sequence 5, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 35, Appli
Sequence 36, Appli
Sequence 19, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 5, Appli
Sequence 16, Appli
Sequence 16, Appli
                                                                              August 30, 2004, 17:02:47 ; Search time 32 Seconds (without alignments) 122.612 Million cell updates/sec
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                                                                                                                                  07330446.PEP
405
1 gpdainapvtccynftnrki......gkwvgdsmdhldkgtgtpkt
                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-716-188-2
US-08-615-232A-5
US-09-197-233-5
US-09-197-233-5
US-09-291-038-5
US-08-310-163-12
US-08-310-163-12
US-08-447-35
US-08-447-494-19
US-08-447-494-19
US-08-447-494-19
US-08-421-144A-5
US-08-421-144A-5
US-08-421-144A-5
US-08-421-144A-5
US-08-421-144A-5
US-08-421-144A-5
US-08-421-19
US-08-421-19
US-08-43-134-24
US-08-43-156A-5
US-08-99-156A-5
US-09-044-855A-5
US-09-186-897A-10
                                                                                                                                                                                                                                                            hits satisfying chosen parameters:
                                                                                                                                                                                                                                  389414 seqs, 51625971 residues
GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match 1
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Perfect score:
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                                                                                 Run on:
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No.
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Patent No. 5212073 Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 30, Appli Sequence 31, Appli Sequence 32, Appli Sequence 32, Appli Sequence 26, Appli Sequence 29, Appli Sequence 19, Appli		92	Length 76;
99 6 5212073-2 76 1 US-07-956-862A-1 76 1 US-08-256-58-1 78 5 PCT-US95-0565-1 69 4 US-09-463-458A-3 69 4 US-09-463-458A-3 69 4 US-09-463-458A-9 68 4 US-09-463-458A-19 76 4 US-09-479-729B-19 76 4 US-09-13-822-19 76 4 US-09-479-729B-19 76 4 US-09-479-729B-19 77 4 US-08-480-483-483-483-483-483-483-483-483-483-483	ALIGNMENTS	n US/08716188 RODNEY W USE OF WCP-1 FOR INDUCING, S: 7 RESS: RTH GLEBE ROAD RTH GLEBE ROAD TO POWDATIBLE C COMPATIBLE C COMPATIBLE C PC-DOS/MS-DOS TH Release #1.0, Version #1. N DATA: N	100.0%; Score 405; DB 2; v 100.0%; Pred. No. 6.1e-47
100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		ULT 1 08-716-188-2 equence 2, Application US/0. equence 2, Application US/0. APPLICANT: KELLY, RODNEY ITLE OF INVENTION: USE TITLE OF INVENTION: THE TORRESPONDENCE: 7 CORRESPONDENCE: 7 COMPUTER: ARLINGTON STATE: WA COMPUTER: IBM PC COMPA SOFTWARE: PATENTION DATA: APPLICATION NUMBER: US FILING DATE: 30-SEP-19 CLASSIFICATION DATA: APPLICATION NUMBER: US FILING DATE: 31-MAR-19 PRIOR APPLICATION DATA: APPLICATION NUMBER: 31 FILING DATE: 31-MAR-19 REGISTRATION NUMBER: 31 APPLICATION NUMBER: 31 APPLICATION NUMBER: 31 FILING DATE: 31-MAR-19 REGISTRATION NUMBER: 31 APPLICATION NUM	ch 1 Similarity
20 20 40 40 40 40 40 40 40 40 40 40 40 40 40		RESULT 1 US-08-716-188-2 Sequence 2, Ag Patent No. 59 GENERAL INFOS TITLE OF IN TORRESPOND STREET: CONDITORY COMPUTER	Query Match Best Local

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Gaps

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Indels

Page

Sequence 5, Application US/08470323A

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1 QPDAINAPVTCCYNFINRKISVQRLASYRRITSSKCPKBAVIFKTIVAKEICADPKQKWV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 405; DB 4; Length 76; Best Local Similarity 100.0%; Pred. No. 6.1e-47; Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              Gequence 5, Application US/09195457

Facent No. 6605702

GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: GOSE, PETER J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
FILE REFERENCE: 550-33
CURRENT FILING DATE: 1998-11-18
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/470,323
PRIOR FILING DATE: 1995-06-14
PRIOR FILING DATE: 1995-06-14
PRIOR FILING DATE: 1995-06-14
PRIOR FILING DATE: 1994-09-14
PRIOR FILING DATE: 1994-09-14
PRIOR FILING DATE: 1994-09-14
PRIOR FILING DATE: 1994-09-14
PRIOR FILING DATE: 1994-04-19
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 11
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US-09-195-457-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 405; DB 2; Length 76; 100.0%; Pred. No. 6.1e-47; tive 0; Mismatches 0; Indels
61 QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 76; Conservative
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single

TYPE: amino acid STRANDEDNESS: si

LENGIH:

MOLECULE TYPE: peptide

US-08-615-232A-5

linear

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1 QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADFKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
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PERLETE PARTICATION US/UR4/U323A

GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: WILLIAMS, TONNING TON US.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: GRIFFITHS-JOHN JOHNSON, DAVID A.
APPLICANT: S50-33
CURRENT FILING DATE: 1994-06-14
EARLIER FILING DATE: 1994-09-14
EARLIER FILING DATE: 1993-09-14
EARLIER FILING DATE: 1993-09-14
EARLIER FILING DATE: 1993-09-14
EARLIER FILING DATE: 1994-04-29
NUMBER: OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: human
US-08-470-323-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5
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CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

ARLINGTON : VIRGINIA

APPLICANT: WLLILAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
NUMBER OF SEQUENCES: 11

Sequence 5, Application US/08615232A Patent No. 5993814

US-08-615-232A-5

GENERAL INFORMATION: APPLICANT: WILLIA

Wed Sep

QPDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV 60 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKBAVIFKTIVAKEICADPKQKWV 60

QDSMDHLDKQTQTPKT 76 61 ООЅМОНГОКОТОТРКТ 76

61

g ò g RESULT 3 US-08-470-323-5

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APPLICANT: Daly, Thomas J.
APPLICANT: Daly, Thomas J.
APPLICANT: LaRosa, Gregory J.
TITLE OF INVENTION: Chemokine-Like Proteins and Methods of TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ODSMDHLDKQTQTPKT 76
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COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-330-163-12
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MEDUM TYPE: Floppy disk

COMPUTER: I BM PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/291,038

FLILING DATE: 14-Apr-199

CLASSIFTCATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/615,232A

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9318984

FILING DATE: 13-AUG-1993

APPLICATION NUMBER: GB 9408602

FILING DATE: 29-APR-1994

ATTORNEY/AGENT INPORMATION:

NAME: WITEON WARNING NAMED TO NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 405; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                JOSE, PETER J.
GRIFFITHS-JOHNSON, DAVID A.
HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 550-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                         Sequence 5, Application US/09291038
Patent No. 6635251
GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/08330163
Patent No. 5656724
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                                          61 QDSMDHLDKQTQTPKT 76
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    QDSMDHLDKQTQTPKT
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US-08-330-163-12
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US-09-291-038-5
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Sequence 12, Application US/08482111

APPLICANT: Daly, Thomas J.
APPLICANT: Daly, Thomas J.
APPLICANT: LaRosa, Gregory J.
TITLE OF INVENTION: Chemokine-Like Proteins and Methods of J. US/ORRESPONDENCE ADDRESS:
OCNERSPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 405; DB 1; Length 78; Best Local Similarity 100.0%; Pred. No. 6.3e-47; Matches 76; Conservative 0; Mismatches 0; Indels
                                                                   STATE: MA

COUNTRY: U.S.A.

ZIP: 0210-2804

ZIP: 0210-2804

ZIP: 0210-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/330,163
FILING DATE: 05-AUG-1994
CLASSIFICATION: 530
ATTORNEY/ACBNT INFORMATION:
REFERENCE/DOCKET NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 00231/080001
TELECHONE: (617) 542-5070
TELECHONE: (617) 542-5070
TELECHONE: (617) 542-5070
INFORMATION FOR SEQ ID NO: 12:
SEQUIENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TWO TO THE TO T
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1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 QPDAINAPVTCCYNFTNRKISVQRLASYRRITISSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTONREY/AGBRT INPORMATION:
NAME: BRIXT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 405; DB 1;
Pred. No. 6.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 405; Dest Local Similarity 100.0%; Pred. No. 6.3 Best Local Similarity 100.0%; Mismatches 7f; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51916/102/INBI
                                                                                                                                                                                   00231/083001
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,111
FILING DATE: 07-UTN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 00231/08300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-127-499A-35
US-08-127-499A-35
Sequence 35, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 орѕмонгокототект 78
                                                                                                                                                                                                                                                                                                                              LENGTH: 78 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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US-08-127-499A-35

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TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                       1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
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                                                                                                                    24 QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
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                                               Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/127,499
FILING DATE: S-SED-1993
ATTORNEY/AGBNT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 51916/104/INBI
Query Match
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                           NG-08-482-847-35
Sequence 35, Application US/08482847
Patent No. 5556757
PAPLICANT: VAN ALSTYNE, Diane
APPLICANT: VAN ALSTYNE, Lawrence Rajendra
APPLICANT: SHARMA, Insurence Rajendra
                                                                                                                                                                                 61 QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                          84 орзмонгркототркт 99
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (202) 672-5300
(202) 672-5399
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SEQUENCE CHARACTERISTICS:
LENGTH: 99 amir.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & La
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US-08-482-847-35
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COUNTRY:
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1 OPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 405; DB 1; Length 99; Best Local Similarity 100.0%; Pred. No. 8.6e-47; Matches 76; Conservative 0; Mismatches 0; Indels
                                        STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 111inois STATE: 111inois COUNTRY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: FIDPPY disk COMPUTER: IBM PC COMPATIBLE OF SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentln Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,449
                                                                                                                                                                                                                                                                                                                                     PPLICATION TO THE PERIOD ATTENDED ATTORNEY AGENT INFORMATION:

CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Gass, David A. REGISTRATION NUMBER: 38,153
REFREENCE DOCKET NUMBER: 27866/32779
TELEPHONE: 312/474-048
TELEPHONE: 312/474-048
INFORMATION FOR SEG
INFORMATION FOR SEG
INFORMATION FOR SEG
INFORMATION FOR SIGH
SEQUENCE CHARACTERISTICS:
LYPE: a mino acid
TYPE: a mino acid
STRANDEDNESS: single
"TYPE: neering acid
STRANDEDNESS: single
"TYPE: neering acid
TYPE: neering acid
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)
OTHER INFORMATION: "Hu MCP-1"
US-08-480-449-19
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                                        Sequence 8, Application US/08347492B
; Setence 8, Application US/08347492B
; Patent No. 5602008
; GENERAL INFORMATION:
; APPLICANT: Wilde, Craig G.
; APPLICANT: Bandman, Olga
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
; TITLE OF SEQUENCES:
; TORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: LBW COMPUTER: DOS COMPUTER: DOS COTRARANES SOFTWARE: FRAKESO Version 1.5 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,492B FILING DATE: 29-NOV-1994

PRIOR APPLICATION NUMBER: 08/30,011

FILING DATE: 07-SEP-1994

APPLICATION NUMBER: 08/30,011

FILING DATE: 05-CCT-1994

ATTORNEY, AGENT INPORMATION: NAME: Luther, Barbara J

REGISTRATION NUMBER: 33,954

REGISTRATION NUMBER: 33,954

REPREMENCE DOCKET NUMBER: 33,954

REPREMENCE DOCKET NUMBER: 33,954

REPREMENCE POCKET NUMBER: 33,954

REPREMENCE POCKET NUMBER: 33,954

REPREMENCE POCKET NUMBER: 33,954

REPREMENTATION NUMBER: 33,954

REPREMENTATION NUMBER: 38,955

JELEPHONE: 415-852-055

JELEPHONE: 415-852-055

RELEPHONE: 415-852-055

SEQUENCE CHARACTERISTICS: LENGTH: 99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: GI 487124
US-08-347-4928-8
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RESULT 10
US-08-347-492B-8
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3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive

0/330440.pep.ral

Wed beb I U8:4/:04 2004

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COMPUTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/NMS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
61 QDSMDHLDKQTQTPKT 76
                 84 ОДЗМДНЕДКОТОТРКТ 99
                                                                                                            24 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKSICADPKQKWV 83
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                                                                                                                                                                         0; Gaps
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                                                                                                                              Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08726830A
Patent No. 5880263
GENERAL INFORMATION:
APPLICANT: LI HADDONG
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: MONOCYTE CHEMOTACTIC PROTEIN-4
NUMBER OF SEQUENCES: 6
CORRESPONDENCE S. 6
CORRESPONDENCE STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 99;
                                                                                                                                                                       Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATE:
LING DATE: US/08/726,830A
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Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                              Query Match
100.0%; Score 405; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION 0475
APPLICATION NUMBER: 08/479,126
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION NUMBER: 08/424,425
FILING DATE: 12-APR-1995
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              61 QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                                                                                                                                        84 ODSMDHLDKQTQTPKT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202-371-2540
        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                               TOPOLOGY: linear; MOLECULE TYPE: protein US-08-421-144A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-726-830A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: COLEMAN ROGER
APPLICANT: STUBAR, SUGAN G.
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DILIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 100.0%; Score 405; DB 2; Length 99; Best Local Similarity 100.0%; Pred. No. 8.6e-47; Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILING DATE: 13.-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGATION:
NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PP-0031 US
TELECOMONICATION: NUMBER: 415-855-0555
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340001
FILECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acide
APPLICATION NUMBER: US/08/479,126B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAMB: STEFFE, BRIC K
REGISTRATION NUMBER: 36,689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 QDSMDHLDKQTQTPKT 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415-855-0555
TELEPAX: 415-85-0195
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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US-08-421-144A-5
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PRETENT NO. 5927103

PREPLICANT: Godiska, Ronald
APPLICANT: Godiska, Petrick M.

TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
TITLE OF INVENTION: ANALOSS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'TOOle, Gerstein, Murray & Borun
CITY: Cidogo
CONTRY: 1011nois
CONTRY: United States of America
STRATE: 1111nois
CONTRY: United States of America
CONTRY: O'TOUR STATES OF STATES
CONTRY: APPLICATION NUMBER: US/08/660,542
FILING DATE: 16NOV-1995
FILING DATE: 18NOVATION: 18NOVATION:
NAME: Gass, David A. 18, 18, 153
REGISTRATION NUMBER: 27866/13318
TELECANION TORR STOLES
TELECANION FOR SEO ID NO: 199
TELECANION FOR SEO ID NO: 199
TELECANION FOR SEO ID NO: 199
TELECANION TORS STOLE O'THE AND STATES O'THE AMERICA
TOPOLOGY: 11nn and COTHER INFORMATION: "HU MCP-1"
FRAITISE: TELECATION: "HU MCP-1"
FRAITISE: PREPIRED STATES: "HIGH GARLING STATUSES: STAINDENDES: STAINDENDE
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Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                RESULT 15
105-08-660-542-19.
Sequence 19, Application US/08660542
Patent No. 5932703...
                                                                                                                                                                    84 QDSMDHLDKQTQTPKT 99
                                                                                                                    61 ODSMDHLDKOTOTPKT 76
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; LOCATION: 1..76
US-08-660-542-19
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61 QDSMDHLDKQTQTPKT 76

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84 QDSMDHLDKQTQTPKT 99
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Search completed: August 30, 2004, 17:08:40 Job time : 35 secs 셤

3 1・4)4・0 1100000

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Wed Seb

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Wed Sep 1 08:47:04 2004

0/330446.pep.rag

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein August 30, 2004, 16:51:56; Search time 122 Seconds (without alignments) 176.013 Million cell updates/sec Run on:

Title: 07330446.PBP Perfect score: 405 Sequence: 1 apdainapvtccynftnrki......gkwyddsmdhldkqtqtpkt 76

Scoring table: BLOSUM62 Gapext 0.5

1586107 segs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp200s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aar28660 MCF. 3/20	0	Aay69030 Amino aci	0 Human	<u>-</u>	8	Adc89673 Human mat	_	Ade80852 huMCP1 ch	_	~	m	Aar73914 Human mon	Aar70800 Chemoattr	4	9	1 Human	Aab15785 Human che	Aab97914 Human mon	0	9 Human	н	Abp65214 Hypoxia-r	σ	Abu10502 Human MCP
07171717170	ΙD	AAR28660	AAR87680	AAY69030	AA020010	AA014143	AAM53048	ADC89673	ADD14998	ADE80852	ADE06777	AAP95387	AAR28663	AAR73914	AAR70800	AAW40174	AAY26176	AAY48391	AAB15785	AAB97914	AAM52440	AAU77179	ABB80901	ABP65214	ABP96799	ABU10502
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æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	•		100.0	Ö	100.0
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Query Match 100.0%; Score 405; DB 2; Length 76; Best Local Similarity 100.0%; Pred. No. 8.7e-43; Matches 76; Conservative 0; Mismatches 0; Indels

Sequence 76 AA;

_	Ade48100 Human mon	Add14997 Human mon	Aay69049 A chemoki	Ø	Aay69051 A chemoki		8				Aaw09374 Monocyte	Aaw11131 Mature hu	Aar86859 Mature MC	Aar87676 (24-Arg)	Aar87677 (3-Ala) M	Aar87675 (28-Asp)	Aay14222 Chemokine	Aar53398 Sense MCP	Adc89672 Human MCP	
ADC89670	ADE48100	ADD14997	AAY69049	AAY69050	AAY69051	AAW40175	AAB12818	ADC89671	AAR06398	AAP90292	AAW09374	AAW11131	AAR86859	AAR87676	AAR87677	AAR87675	AAY14222	AAR53398	ADC89672	
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66	66	122	325	N	332	76	97	77	66	16	, 9/	92	77	16	16	16	77	16	77	
100.0	100.0	100.0	100.0	100.0	100.0	99.3	99.3	0.66	0.66	98.8	ω,	8.86	00	ထ	98.0	97.5	96.5	0.96	0.96	
405	405	405	405	405	405	402	402	401	401	400	400	400	400	397	397	395	391	688	389	
56	27	28	5 2		31	3	33	ж 4	35	36	3.7	80	6 8	40	4.	42	43	4 4	45	

ALIGNMENTS

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Chemokine receptor; ligand; inflammatory response; immune effector cell; secondary tissue damage; central nervous system injury; MCP-1; CNS inflammatory disease; neurodegenerative disorder; heart disease; inflammatory bowel disease; inflammatory kidney, renal disease; inflammatory kidney, renal disease; inflammatory kidney, renal disease; inflammatory hasal disease; inflammatory hasal disease; inflammatory that disease; inflammatory hasal disease; inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a chemokine receptor ligand. The present ligand can be incorporated into the conjugates of the invention. The specification describes a conjugate, comprising a targeted agent and a chemokine receptor ligand. The conjugate binds to a chemokine receptor resulting in internalisation of the targeted agent in cells bearing the receptor. The conjugates are used for formulating a medicament or for treating disorders associated with inflammatory responses resulting from activation, proliferation and migration of immune effector cells. The disorders or disease states comprise secondary tissue damage such as central nervous system (CNS) injury, CNS inflammatory diseases, inflammatory hard diseases, inflammatory point diseases, inflammatory nasal diseases, inflammatory lung diseases, inflammatory nasal diseases, inflammatory lung diseases, inflammatory nasal diseases, inflammatory thyroid diseases such as thyroiditis, or cytokine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A new therapeutic agent comprising a conjugate for treating secondary tissue damage and other disease conditions like Alzheimer's disease, stroke, Parkinson's disease and atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Pred. No. 8.7e-43;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human chemokine MCP-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                          (OSPR-) OSPREY PHARM LID,
                                                                                                                                                                                                                                                                                                                                                                                                                   Coggins PJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-182542/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 76 AA;
                                                                                                                                                                                                           WO200004926-A2
                                                                                                                                                                      domo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                 Mcdonald JR,
                                                                                                                                                                                                                                                                                            21-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising a growth factor, comprises a monocyte chemotactic activating factor (MCAF) or its variants or derivatives. The factor has potent effect on skin wounds and ulcers. The present sequence is human MCAF, the activity of which is exemplified as the new remedy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new remedy for curing wounds which, instead of
    9
                       QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIPKTIVAKEICADPKQXWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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  QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
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                                                                                                                                                                                                                                                                                                                                                  Monocyte chemotactic activating factor for use as wound remedy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monocyte chemotactic factor - has potent
skin wounds and ulcers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 76;
                                                                                                                                                                                                                                                                                                                                                                                         monocyte chemotactic activating factor; MCAF; wound remedy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 405; DB 2;
100.0%; Pred. No. 8.7e-43;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 12; 22pp; Japanese.
                                                                                                                                                                                                                          AAR87680 standard; protein; 76 AA.
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                                                                                QDSMDHLDKQTQTPKT
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therapeutic effect on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-131181/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TORA ) TORAY
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AAR87680
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Sequence 76 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM53048;
                                Offord R,
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
AAM53048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chemokine receptor modulator; chemokine; HIV infection; AIDS; asthma; allergic rhinitis; atopic dermatitis; atheroma; antiinflammatory; antiastlergic; dermatological; antiarteriossclerotic; antirtheumatic; antiatheriosalpatesive; MCP-1; atherosclerosis; organ transplant rejection; rheumatoid arthritis.
                                                                                                                                                                                                                                                                  The invention relates to polymer-modified bioactive synthetic chemokines and to methods for their production and use. The compounds and methods of the backbone of the invention are useful in the analysis and treatment of various diseases states e.g. HIV and AIDS related disorders, asthma, allergic rhinitis, atopic dermatitis, atheroma/atheroma/atherosis, organ transplant rejection, and rheumatoid arthritis. This sequence represents the human chemokine MCP-1 protein of the invention
immunosuppressive; polymer-modified bioactive synthetic chemokine; HIV; AIDS; asthma; allergic rhinitis; atopic dermatitis; rheumatoid arthritis; atheroma; atherosclerosis; organ transplant rejection; MCP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                     1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QPDAINAFVTCCYNFTNRKISVQRLASYRRITSSKCPKBAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                New polymer-modified bioactive synthetic chemokines useful in the treatment of various diseases or disorders e.g. asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                       Chen S,
                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 405; DB 5;
100.0%; Pred. No. 8.7e-43;
ive 0; Mismatches 0;
                                                                                                                                                                        Bradburne JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA014143 standard; protein; 76 AA.
                                                                                                                                                                                                                                                Claim 8; Fig 10A; 176pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2000; 2000US-0217683P.
                                                                                                          12-JUL-2001; 2001WO-US021933.
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                                                                                                                              12-JUL-2000; 2000US-0217683P
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
----- 76; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human MCP-1 protein.
                                                                                                                                                                                             WPI; 2002-268857/31.
                                                                                                                                                   (GRYP-) GRYPHON SCI
                                                                                                                                                                        Kochendoerfer G,
                                                                 WO200204015-A1.
                                                                                                                                                                                                                                                                                                                                                         Sequence 76 AA;
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                                                                                     17-JAN-2002
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                                                                                                                                                                                                                                                                                                              The present invention relates to chemokine receptor modulators, which comprise a chemokine polypeptide chain modified at N-terminus with an aliphatic chain and at least one amino acid derivatives and/or modified at its C-terminus with an aliphatic chain or polycyclic. The modulators can be used to treat diseases such as HIV infection, AIDS, asthma, allergic fininits, atopic dermatitis, atheroma, atherosclerosis, organ transplant rejection and rheumatoid arthritis. The present sequence is the human MCP-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, monocyte chemoattractant protein-1, MCP-1, C-C chemokine family, pulmonary hypertension, primary, hypotensive.
                                                                                                                                                        Chemokine receptor modulator useful for treating e.g. asthma, allergic rhinitis comprises a chemically modified carboxyl-terminus and/or amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QPDAINAFVTCCYNFTNRKISVQRLASYRRITSSKCFKEAVIFKTIVAKBICADFKQKWW
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/note= "These residues are deleted in a specifically
claimed human MCP-1 miteart, 7ND-MCP-1 (AAM53049)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human monocyte chemoattractant protein-1 (MCP-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 405; DB 5;
100.0%; Pred. No. 8.7e-43;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM53048 standard; protein; 76 AA.
                                                    Hartley 0;
                                                                                                                                                                                                                                                                           Example 3; Fig 2; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2001; 2001WO-JP004381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ODSMDHLDKQTQTPKT 76
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Best Local Similarity 100...
Best Accal Similarity 100...
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                                                 Gaertner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-083059/11.
N-PSDB; ABA02497.
(GRYP-) GRYPHON SCI
                                                                                                         WPI; 2002-171703/22
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                                                                                                                                                                                                                         terminus analogs.
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Glutamic Acid or Glutamine: 18 and 19; 18 and/or 19, together with 58; 18 and/or 19, together with 66; 18 and/or 19, together with 66; 18 and/or 19, together with 66; 18 and/or 19, together with 24, 44, 49 and/or 75. A protein of the invention has immunosuppressive, antiinflammatory, cytostatic, antimicrobial, and vasotropic activity. The protein may have a use in gene therapy, and in a vaccine. The MCP proteins are human MCP-1, human MCP-2, human MCP-3, human MCP-4 or human Botaxin. The MCP anteagonists are useful in preparing a composition for treating or preventing diseases traladed to excessive leukocyte migration and activation, e.g., vascular disorders, cancer, inflammatory or autoimmune disease or infection. The present sequence is used in the exemplification of the invention.

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Sequence 76 AA;

Length 76; Indels

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hypertension, comprising an antegonistic inhibitory mutant of monocyte chemoattractant protein-1 (MCP-1), DNA encoding the mutant MCP-1, or a neutralising antibody against MCP-1. DNA encoding the mutant MCP-1, or a chemokine family. The preventives and remedies have hypotensive activity and can be used in the prevention and treatment of pulmonary hypertension particularly pulmonary primary hypertension. The present sequence
Preventives and remedies for pulmonary hypertension containing mutant of MCP-1 antagonistic inhibitory type or its salt, encoded DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; MCP-1; monocyte chemoattractant protein; MCP; immunosuppressive; antiinifalmmatory; oytostatic; antimicrobial; vasotropic; gene therapy; MCP-2; MCP-4; Ectaxin; leukocyte migration; leukocyte activation; vascular disorder; cancer; inflammatory; autoimmune disease; infection.
                                                                                                                                                                                                   The invention relates to preventives and remedies for pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 405; DB 5;
100.0%; Pred. No. 8.7e-43;
tive 0; Mismatches 0;
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                                                                                                                               Page 31; 39pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-2002; 2002US-0371442P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76; Conservative
                               MCP-1 antagonistic inhil neutralization antibody
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 76 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Enhancing biocompatibility of a medical device implanted in a portion of a living body by contacting the portion of the body that is in contact with the implanted device with monocyte chemoattractant protein 1 (MCP-1)
                                                                                                       1 QPDAINAPVICCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPRQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a medical device implanted within a portion of a living body comprising contacting a portion of the living body in contact with the device with a monocyte chemoattractant protein 1 (MCP-1) antagonist to inhibit chronic inflammation induced by the presence of the medical device or fibrous encapsulation of the medical device. The method is useful for enhancing the biocompatibility of a medical device implanted in a portion of a living body by inhibiting chronic inflammation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a method of enhancing (M1) the biocompatibility
                                                                              1 OPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory; MCP-1 Antagonist; biocompatibility; medical device; monocyte chemoattractant protein 1; MCP-1; MCP-1 antagonist; chronic inflammation; fibrous encapsulation; human.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Human monocyte chemoattractant protein-1 (MCP-1) mature protein.
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0
  Length 76;
                                      Indels
Score 405; DB 7;
Pred. No. 8.7e-43;
); Mismatches 0;
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100.0%; Sc
100.0%; Pr
:ive 0;
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                                                                                                                                                                                                                                                                                                                                                                             15-JAN-2004 (first entry)
                                                                                                                                                              61 ODSMDHLDKOTOTPKT
                                                                                                                                                                                              61 ODSMDHLDKQTQTPKT
Query Match
Best Local Similarity 100.
Matches 76; Conservative
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N-PSDB; ADD14996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                         ADD14998;
                                                                                                                                                                                                                                                           RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antagonists of MCP proteins, useful in preparing a composition for treating or preventing diseases related to excessive leukocyte migration and activation e.g. vascular, inflammatory or autoimmune disease, cancer or infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel antagonists of MCP proteins comprising mutants of MCP proteins in which the following combinations of residues, numbered on the sequence of human mature MCP-1, are substituted to Alanine, Glycine, Serine, Threonine, Proline, Aspartic Acid, Asparagine,
                                                                                                   Gaps
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Handel T;

Example 3; SEQ ID NO 4; 63pp; English.

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WO2003083059-A2.
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                                                                                                                     29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                   Heavner GA,
                                                                                                ADE06777;
   61
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                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating
                                                                                                            9
                                                                                                                      1 QPDAINAPVTCCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
formation of fibrous capsules around the device. This is the amino acid sequence of human monocyte chemoattractant protein-1 (MCP-1) mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPDAINAPVTCCYNFTNEKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                        1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nuclear targeting peptide comprising a nuclear targeting domain isolated from a chemokine, useful for preparing a medicament for tre cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma.
                                                                                                                                                                                                                                                                                                                Nuclear targeting peptide; nuclear targeting domain; ESkine; PESKY; chemokine; cancer; cytostatic; huMCP1; chemokine.
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0
                                                                Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 76;
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                              Score 405; DB 7;
Pred. No. 8.7e-43;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 405; DB 7;
100.0%; Pred. No. 8.7e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 11, 66pp, English.
                                                                                                                                                                                                                            ADE80852 standard; peptide; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CANC-) CANCER RES TECHNOLOGY LTD.
                                                              100.0%; Sc
100.0%; Pr
cive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     02-APR-2002; 2002GB-00007624.
                                                                                                                                                    26
                                                                                                                                                                                                                                                                                                                                                                                                                 2003WO-GB001472.
                                                                                                                                                                    QDSMDHLDKQTQTPKT
                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                   61 QDSMDHLDKQTQTPKT
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                  Query Match
Best Local Similarity
Lag 76, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
76; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-788341/74.
                                                                                                                                                                                                                                                                                           huMCP1 chemokine.
                                                                                                                                                                                                                                                                                                                                                                      WO2003082920-A1.
                                          Sequence 76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention
                                                                                                                                                                                                                                                                                                                                                                                                                 02-APR-2003;
                                                                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graham G;
                                                                                                                                                                                                                                                  ADE80852
                     protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New monocyte chemoattractant protein-1 (MCP-1) mutein nucleic acid, useful for diagnosing or treating a MCP-1 mutein-related condition, e.g. immune, cardiovascular, neurologic or infectious or malignant disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                human; MCP-1; monocyte chemoattractant protein-1; immunosuppressive; cardiant; neuroprotective; antimicrobial; cytostatic; gene therapy; immune disorder; cardiovascular disorder; neurological disorder; infectious disorder; malignant disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
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100.0%; Pred. No. 8.7e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1; 81pp; English.
                                                                                                                                                              ADE06777 standard; protein; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002; 2002US-0367932P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAR-2003; 2003WO-US009056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
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61 ODSMDHLDKOTOTPKT
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ODSMDHLDKOTOTPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ОВЗМВНІВКОТОТРКТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                   Human MCP-1 SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CENZ ) CENTOCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-804039/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Das A;
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07330446.pep.rag

(revised)
(first entry)

17-DEC-2001 25-JUL-1989

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An expression plasmid, pHMC076 for producing MCF(76) consisting of 76 amino acids was constructed. DNA encoding MCF(76) was prepd. using a recombinant plasmid pHMCF7. (Updated on 25-MAR-2003 to correct PN field.)
           Plasmid, monocyte chemotactic factor; MCF; translation; termination; terminator; initiation; ribosome binding site; RBS; promoter; tryptophan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 QPDAINAPVTCCYNFINRKISVQRLASYRRITSSKCFKEAVIFKTIVAKEICADPKQKWV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodn. of polypeptide(s) having monocyte chemotactic activity - using expression plasmids with E. coli elements and specific E.coli strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKIIVAKEICADPKOKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human monocyte chemoattractant factor; hMCP-1; chemokine; vaccine; meningitis related homologous antigenic sequence; MRHAS; RV-1; immunoassay; diagnosis; treatment; prophylactic; bacterial; viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human monocyte chemoattractant factor hMCP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                       Fukui T, Yamada M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 43-44; 56pp; English.
                                                                                                                                        1. .23
/label= sig_peptide
24. .99
/label= mat_protein
                                                                                                                        cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR73914 standard; protein; 99 AA.
                                                                                                                                                                                                                                                                                                                                                                                  (DAIN ) DAINIPPON PHARM CO LTD
                                                                                                                                                                                                                                                                                                          92WO-JP000550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 QDSMDHLDKQTQTPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ODSMDHLDKOTOTPKT
                                                                                                                                                                                                                                                                                                                                                                                                                       Matsuo N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-398864/48.
N-PSDB; AAQ30748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       /amagishi J,
                                                                                                                                                                                                                                                                                                             27-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                     409219737-A1
                                                                                                                                                                                                                                                                                                                                                09-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
05-DEC-1995
                                                                                                                                                                                                                                                                      12-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-1995
                                                      repressor.
                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR73914;
                                                                                                                            Key
Peptide
                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
AAR73914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is a human-derived monoyte chemo-attractant peptide (MCP-1) sequence mol. mass of c.a. 8,400 D. MCP-1 can be used for treating infection eg inflammatory disease, or for the control of neoplasms by accumulation of monocytes at the site of the infection. The corresp. DNA is obtd. by chemical synthesis, by screening reverse trascripts of mRNA from purified blood leukcytes or cell cultures of eg U-373 MG or KMG-E. (Note: Revised entry submitted to correct the patent number format of US Government-numbers. For further information please with negoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human derived monocyte chemo:attractant peptide prods. - obtd. from human glioma cell line U-105MG or peripheral blood mono:nuclear leukocytes.
                                                                                       Human monocyte chemo-attractant peptide; inflammatory disease; neoplasms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QPDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKQKWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leonard EJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 405; DB 1;
100.0%; Pred. No. 1.2e-42;
tive 0; Mismatches 0;
                                                      Human monocyte chemo-attractant peptide-1.
                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICE.
(USDC ) US SEC OF COMMERCE.
(USDC ) US SEC OF COMMERCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robinson EA, Appella E,
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR28663 standard; protein; 99 AA.
                                                                                                                                                                                 24. .99
/product= "MCP-1"
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Disclosure; Fig 2; 66pp; English.

WPI; 1989-300683/41.

Yoshimura T,

N-PSDB; AAN91337

89US-00330446

30-MAR-1989; 31-JAN-1989;

25-JUL-1989

USN7330446-N.

Protein

Homo sapiens

89US-00304234

92

QDSMDHLDKQTQTPKT QDSMDHLDKQTQTPKT

61

Local Similarity 100. les 76; Conservative

Matches

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correct PA field.

Sequence 99 AA;

Query Match

9

(revised)
(first entry)

25-MAR-2003 24-MAR-1993

MCF.

AAR28663;

AAR28663 ID AAR2 XX AAR2 AC AAR2 XX DT 25-W DT 24-W XX DE MCF.

RESULT 12

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Gaps

; 0

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Screening for cpds. with anti-heparanase activity - by detecting inhibition of heparan or heparan sulphate degradation, potentially useful for treating arthritis, restenosis, cancer.
   N-PSDB; AAQ85370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV10341.
                                                                                                                                                                                   Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-1989;
30-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leonard EJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                      AAW40174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
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   RXFFFXXXX000000XX
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                                                                                                                                                                                                                AAR73914 is the chemokine Human monocyte chemoattractant factor hMCP-1. It contains the meningitis related antigenic sequences (MRHAS) claimed in AAR73895 and AAR73807, which are recognised by a monoclonal antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be used in immunoassays to diagnose the presence of bacterial and/or viral meningitis agents in a sample, or in prophylactic and therapeutic meningitis Lreatments. The peptides may also be used as vaccines against (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                   1 OPDAINAPUTCCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   24 QPDAINAPVTCCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKAV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemoattractant; heparanase; heparin; heparan sulfate; arthritis;
                                                                                                                      New peptide(s) and corresp, antibodies for the treatment of meningitis the peptide(s) corresp. to homologous antigenic sites on bacterial and viral agents and on chemokine(s), used for detecting and preventing meningitis.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                      Length 99;
                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 405; DB 2; Length 9
100.0%; Pred. No. 1.2e-42;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                            Claim 47; Fig 8/10; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restenosis; cancer; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR70800 standard; protein; 99 AA.
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94WO-CA000516.
                       93US-00127499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ODSMDHLDKOTOTPKT 99
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93US-00136117
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                                                                                    LR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100..
Local Similarity 100..
                                                                                   Sharma
                                                ö
                                              (VALS/) VAN ALSTYNE
                                                                                                          WPI; 1995-147431/19.
                                                           (SHAR/) SHARMA L R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ဗ
                                                                                 Van Alstyne D,
                                                                                                                                                                                                                                                                                                                                            Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NHODAN ( ODAN)
28-SEP-1994;
                       28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoogwerf AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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29-AUG-1995
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WPI; 1995-082239/11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monocyte chemoattractant peptide; MCP; MCP-1; treatment; neoplasm; infection; human; monocyte receptor; chemotactic response; inflammation; monocyte infiltration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a monocyte chemoattractant peptide (MCP) designated MCP-1. MCPs can be isolated from human glioma cell line U-
                           Purified heparanases, prepared under reducing conditions and activated with transglutaminase, are given in AAR70786-804. Most are prepared by reverse transcription of mRNA from activated human leukocytes, then cloning of the cDNA into pVL1392 baculovirus vector, and expression in $f9 cells in the presence of reduced glutathione and dithiothreitol. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                               24 QPDAINAPVICCYNFINRKISVQRLASYRRIITSSKCPKEAVIFKTIVAKEICADPKOKWV
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37. .39
/note= "potential N-linked glycosylation site"
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glioma cells, useful for treating infections and neoplasms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macrophage chemoattractant peptide designated MCP-1.
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100.0%; Pred. No. 1.2e-42;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAW40174 standard; protein; 99 AA.
Claim 13; Page 49; 60pp; English.
                                                                                                                                                                                                                                                                                                                             84 QDSMDHLDXQTQTPKT 99
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89US-00330446
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Best Local Similarity 100...
To, Conservative
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CC treatment of neoplasms and infections in humans. Short peptides derived creatment of neoplasms and infections in humans. Short peptides derived creeptor without stimulating a chemotactic response. These are coperated in the form treating inflammation associated with monocyte coperatially useful for treating inflammation associated with monocyte compliance of the form treating inflammation associated with monocyte compliance of the follows: Score 405, DB 2; Length 99; Cuery Match 20, Conservative 0, Mismatches 0; Indels 0, Gaps 0; Matches 76; Conservative 0, Mismatches 0; Indels 0, Gaps 0; Coperation 10, DB 10, Mismatches 0, Indels 0, Gaps 0; Matches 10, DB 24 QPDAINAPVICCYNFTNRKISVQRIASYRRITSSKCPKEAVIFKTIVAKEICADPRQKWW 83
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Search completed: August 30, 2004, 17:04:49
Job time : 126 secs

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August 30, 2004, 17:07:28 ; Search time 129 Seconds (without alignments) 185.353 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO'_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUBL_pep:*
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7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score: 4
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 5, Appli	Sequence 20, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 20, Appl	Sequence 5, Appli	Sequence 7, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 210, App	Sequence 16, Appl	Sequence 9, Appli	Sequence 5, Appli	Sequence 395, App	Sequence 9, Appli
	QI	US-09-195-457-5	US-09-792-793A-20	US-10-339-778-3	US-10-276-971-1	US-10-375-209A-20	US-10-332-038A-5	US-10-668-733-7	US-10-668-733-14	US-10-803-960-14	US-10-449-831A-210	US-08-927-939-16	US-09-920-137A-9	US-10-054-967-5	US-10-170-385-395	US-10-057-275-9
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Sequence 4, Appli Sequence 9, Appli Sequence 9, Appli Sequence 22, Appli Sequence 22, Appli Sequence 18, Appli Sequence 71, Appli Sequence 71, Appli Sequence 71, Appli Sequence 72, Appli Sequence 73, Appli Sequence 73, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 19, Appli	equence 6,
US-10-033-067-4 US-10-141-965-5 US-10-141-965-6 US-10-293-705-8 US-10-137-655-9 US-10-137-655-9 US-10-137-655-9 US-10-137-78-2 US-10-34-464-62 US-10-34-778-2 US-10-34-778-2 US-10-375-209A-71 US-09-792-793A-71 US-09-792-793A-71 US-09-792-793A-73 US-10-375-209A-72 US-10-375-209A-72 US-10-375-209A-72 US-10-375-209A-72 US-10-375-209A-72 US-10-375-209A-73 US-10-375-209A-73 US-10-375-209A-73 US-10-375-209A-73 US-10-339-778-4 US-10-339-778-4 US-10-276-971-2 US-10-276-971-2 US-10-276-971-2 US-10-137-655-5 US-10-137-655-5 US-10-137-655-5 US-10-137-655-5 US-10-125-451-19 US-10-125-451-19 US-10-125-451-19 US-10-125-451-19 US-10-125-451-19	-10-332-038A-6
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ALIGNMENTS

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US-10-375-209A-20

Sequence 20, Application US/10375209A

Sequence 20, Application US/10375209A

Sequence 20, Application US/2016421A1

Sequence 20, Application US/2016421A1

GENERAL INFORMATION:

APPLICANT: Coggins, Philip

APPLICANT: Coggins, Philip

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

TITLE OF INVENTION: UNMER: US/10/375,209A

CURRENT APPLICATION NUMBER: US/10/375,209A

CURRENT FILING DATE: 2003-02-24

NUMBER OF SEQ ID NOS: 93

SOCTWARE: Patentin Ver. 2.0

SEQ ID NO SEQ ID NOS: 93

LENGTH: 76
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                                  Sequence 1, Application US/10276971

Publication No. US20030162737A1

GENERAL INFORMATION:

APPLICANT: Egashira Kensuke

APPLICANT: Yoshikazu Yonemitsu

APPLICANT: Yashira Ineda

APPLICANT: Yashira Ineda

TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
FILE REFERENCE: 2733 USOP

CURRENT APPLICATION NUMBER: US/10/276,971

CURRENT FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 4
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Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels (
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; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-10-375-209A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 405; DB 14; Best Local Similarity 100.0%; Pred. No. 4.6e-43; Matches 76; Conservative 0; Mismatches 0;
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ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
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                                                                                                                 Sequence 20, Application US/09792793A

Patent No. US20020168370A1

Patent No. US20020168370A1

APPLICANT: NROAMINION:
APPLICANT: Coggins, Philip

APPLICANT: Coggins, Philip

APPLICANT: Coggins, Philip

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REFERENCE: 25020-601D

CURRENT APPLICATION NUBBR: US/09/792,793A

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20

LENGTH: 76
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APPLICANT: Bornstein, P.
APPLICANT: Kyriakides, T.
TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC TITLE OF INVENTION: DEVICE FILE REPERENCE: UWGNIT-1-2025
CURRENT APPLICATION NUMBER: US 60/347,560
PRIOR APPLICATION NUMBER: US 60/347,560
PRIOR FILING DATE: 2002-01-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NOS: 4
LENGTH: 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 405; DB 9; Length 76; Best Local Similarity 100.0%; Pred. No. 4.6e-43; Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-09-792-793A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10339778 Publication No. US20030129214A1 GENERAL INFORMATION:
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61 QDSMDHLDKQTQTPKT
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US-10-339-778-3
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ORGANISM: homo sapien
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Best Local Similarity
Matches 76; Conserv
                                                                            RESULT 2
US-09-792-793A-20
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; Publication No. US20040138422A1
; GENERAL INPORMATION:
; GENERAL INPORMATION:
; APPLICANT; Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT FILING DATE: 2003-99-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; RION REILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
LENGTH: 76
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APPLICANT: Gryphon Therapeutics, Inc.
APPLICANT: Offord, Robin
APPLICANT: Offord, Robin
APPLICANT: Offord, Robin
APPLICANT: Hartley, Oliver
TITE OF INVENTION: Chemokine Receptor Modulators, Production and Use
FILE REFERENCE: 03504_271
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US 60/217,683
PRIOR PLING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE PATENT OF SEQ ID NOS: 28
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Best Local Similarity 100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels
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100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels
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; LOCATION: (75)...(75)
; OTHER INFORMATION: The Lysine at position 75 is biotinylated
US-10-668-733-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
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; ORGANISM: Homo Sapiens
US-10-332-038A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-668-733-7
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RESULT 8 US-10-668-733-14

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Sequence 14, Application US/10668733

Publication No. US20040138422A1

GENERAL INFORMATION:

APPLICANT: Demotz et al.

TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS

FILE REFREENCE: 2954/38772A

CURRENT APPLICATION NUMBER: US/10/668,733

CURRENT APPLICATION NUMBER: US 60/412,866

PRIOR FILING DATE: 2003-09-23

NUMBER OF SEQ ID NOS: 21

SOFTWARE: Patentin version 3.2

SOFTWARE: Patentin version 3.2

LENGTH: 76
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APPLICANT: White, John R.
APPLICANT: Pelus, Louis
APPLICANT: Pelus, Louis
APPLICANT: Fil, Hacdong
APPLICANT: Kreider, Brent L.
TILE OF INVENTION: NOVEL Chemokine for Mobilizing Stem Cells
FILE REFERENCE: PF497D2
CURRENT FILING DATE: 2004-03-19
FRIOR FILING DATE: 2004-03-19
PRIOR FILING DATE: 2006-05-09
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1999-01-06
PRIOR FILING DATE: 1996-10-24
PRIOR FILING DATE: 1996-10-24
PRIOR FILING DATE: 1996-10-23
PRIOR FILING DATE: 1996-10-23
SOFTWARE: PALENTION NUMBER: US 60/006,051
PRIOR APPLICATION NUMBER: US 60/006,051
PRIOR PELING DATE: 1996-10-23
SOFTWARE: PALENTING DATE: 1996-10-23
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Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 405; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Synthetic peptide US-10-668-733-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/10803960; Publication No. US20040156822A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 QDSMDHLDKQTQTPKT 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QDSMDHLDKQTQTPKT 76
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ORGANISM: MCP-1
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US-10-803-960-14
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APPLICANT: Coleman, Roger
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Wilde, Crain GENOKINES EXPRESSED IN PANCREAS
TITLE OF INVENTION : NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-920-137A-9
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                                                                                                                                                                   STREET: Particular STATE: C
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                                                                                      Sequence 210, Application US/10449831A
Publication No. US20040029179A1
GENERAL INFORMATION:
APPLICANT: Koentgen,
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
FILE REPERENCE: 2385978
CURRENT APPLICATION NUMBER: US/10/449,831A
CURRENT FILING DATE: 2003-05-30
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 237
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Grainger, David J.
APPLICANT: Grainger, David J.
TITLE OF INVENTION: Compounds and methods to inhibit or
TITLE OF INVENTION: augment an inflammatory response.
TITLE REFERENCE: 295.022US1
CURRENT APPLICATION NUMBER: US/08/927,939
CURRENT FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 83
SEQ ID NOS: 83
SEQ ID NO 16
LENGTH: 99
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100.0%; Pred. No. 6.2e-43;
iive 0; Mismatches 0;
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18-08-227-939-16
Sequence 16, Application US/08927939
Publication No. US20010006640A1
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Matches 76; Conservative
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US-08-927-939-16
                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Human
US-10-449-831A-210
                                                                       JS-10-449-831A-210
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 210
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Sequence 9, Application US/09920137A Publication No. US20030049725A1 GENERAL INFORMATION:

US-09-920-137A-9

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1 QPDAINAPVICCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
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OLSEN, HENRIK S.
TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 99;
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       SOFTWARE: FastESG Version 1.5
SOFTWARE: FastESG Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/920,137A
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFESTENCE/DOCKET NUMBER: 9F-0027 US
TELEPHONE: 415-955-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-054-967-5
Sequence 5, Application US/10054967
Publication No. US20030059874A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KREIDER, BRENT L.
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 QDSMDHLDKQTQTPKT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 Орѕмригркототект 76
                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: MCP-1
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Palo Alto
                                             u.s.
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9

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24 QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 83
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                           1 OPDAINAPVICCYNFINRKISVORLASYRRITSSKCPKBAVIFKTIVAKEICADPKOKWV
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0
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Coleman, Roger
APPLICANT: Coleman, Olgan
Wilde, Craig G,
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/057,275
FILING DATE: S2-Gan-2002

PRIOR APPLICATION NUMBER: US/08/390,740A

PLING DATE: PEBLUARY 17, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Lither, Barbara J.

REGISTRATION NUMBER: 33,954

REGISTRATION NUMBER: PF-0027 US

TELECOMMUNICATION INFORMATION:

TELERAX: 415-85-0555

TELERAX: 415-85-0555

TELERAX: 415-85-0555

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 9: US-10-057-275-9
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                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/10057275; Publication No. US20020155545A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ODSMDHLDKOTOTPKT 76
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                                                                                                                                61 ODSMDHLDKOTOTPKT
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STATE: CA
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US-10-057-275-9
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100.0%; Score 405; DB 12; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,967
FILING DATE: 25-Jan-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/995,156
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: 60/042,269
FILING DATE: 31-DEC-1997
APPLICATION NUMBER: 60/042,269
FILING DATE: 31-MR.1997
ATORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
RECLESTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-1/U-385-39

US-10-1/U-385-39

PUDIICACION NO. US20030203372A1

GENERAL INFORMATION:

APPLICANT: Ward, Neil Raymond

APPLICANT: Kan, On

APPLICANT: Harris, Robert Alan

APPLICANT: Harris, Robert Alan

APPLICANT: White, Jonathan

APPLICANT: Sayner, William Nigel

APPLICANT: Rayner, William Nigel

APPLICANT: Rayner, William Nigel

APPLICANT: Rayner, William Nigel

APPLICANT: Kingsman, Susan Mary

APPLICANT: Rayner, William Nigel

CURRENT RILING: 200-01662

PRIOR PILING DATE: 2002-04-08

PRIOR PILING DATE: 2002-04-08

PRIOR PILING DATE: 2002-04-08

PRIOR PILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 549

SEQ ID NO 395

LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-054-967-5
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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, ORGANISM: Homo Sapiens
US-10-170-385-395
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 30, 2004, 16:52:21 ; Search time 24 Seconds

(without alignments)

164.889 Million cell updates/sec
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(without alignments)

Title: 07330446.PBP

Perfect score: 405
Sequence: 1 gpdainapytccynftnrki......gkwyddsmdhldkgtgtpkt 76

Sequence: 1 qpdainapvtccynttnrki...
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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í	a :	SYO	SYO	SYO	SYO	MCP	SY02	MCPB	SXO	SY12	EOI	SYO	SXO	SY1	SX0	SXO	SYO	SYO	EOT	EOT	EOT	SYO	SY07	SYO	SY2	REG1	SY3L	SYO3	SYZ	SY04	SY04	SY04	SY04	SYDI
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SYD1_MOUSE SY04_MOUSE	SY21_HUMAN SY03_RAT SY14_HUMAN	SYD1_HUMAN SY03_MOUSE	SY26_HUMAN SY05_SIGHI	SY18_HUMAN SY05_CAVPO	SY05_BOVIN
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8 8 4 8	33 3 33 4 34 4	€ 4 9 0	41.42	4. 4. 6. 4.	4. U

ALIGNMENTS

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processed form.";
Biochem. Biophys. Res. Commun. 167:904-909(1990).
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       TISSUE=Paroreas;

WEDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

REDLINE=22388257; PubMed=12477932;

RIAUGHER R.D., Colling F.S., Wagner L., Shemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mulahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Galbes R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-91301709; PubMed-2071154;
Rollins B.J., Morton C.C., Ledbetter D.H., Eddy R.L. Jr., Shows T.B.;
"Assignment of the human small inducible cytokine A2 gene, SCYA2
(encoding JE or MCP-1), to 17q11,2-12: evolutionary relatedness of cytokines clustered at the same locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robinson E.A., Yoshimura T., Leonard E.J., Tanaka S., Griffin P.R., Shabanowitz J., Hunt D.F., Appella E., "Complete amino acid sequence of a human monocyte chemoattractant, a putative mediator of cellular immune reactions.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 29-53 AND 82-92.

MEDLINE-90211336; PubMed=232286;.

MEDLINE-90211336; PubMed=232286;.

MEDLINE-90211336; PubMed=232286;.

Midentification of the monocyte chemotactic protein from human osteosarcoma cells and monocytes: detection of a novel N-terminally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20374005; PubMed=10918580;
Finzer P., Soto U., Delius H., Patzelt A., Poustka A., Coy J.F.,
Zur Hausen H., Roesl F.;
"Differential transcriptional regulation of the
monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and
non-tumorigenic HPV 18 positive cells: The role of the chromatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. taken with the state of t
                                                                                                     "The expression of monocyte chemotactic protein (MCP-1) in human vascular endothelium in vitro and in vivo.";
Mol. Cell. Biochem. 126:61-68(1993).
MEDLINE=94150478; PubMed=8107690;
Li Y.S., Shyy Y.J., Wright J.G., Valente A.J., Cornhill J.F.,
Kolattukudy P.E.;
                                                                                                                                                                                                                                                                                                                                             in monocyte chemoattractant protein-1 (MCP-1).";
Exp. Med. Biol. 305:47-56(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        putative mediator of cellular immune reactions.";
Proc. Natl. Acad. Sci. U.S.A. 86:1850-1854(1989).
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=92095166; PubMed=1661560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 24-99.
MEDLINE=89184525; PubMed=2648385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure and AP-1 composition.";
                                                                                                                                                                                                                                                                                                                              Yoshimura T., Leonard E.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 19:3235-3244 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 10:489-492(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=20374005; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            "Human monocyte
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94253189; PubMed=8195247; Zhang Y.J., Rutledge B.J.; Rollins B.J.; Rollins B.J.; Rutledge B.J., Rollins B.J.; Rutledge Cartivity analysis of human monocyte chemoattractant protein-1 (MCP-1) by mutagenesis. Identification of a mutated protein that inhibits MCP-1-mediated monocyte chemotaxis."; J. Biol. Chem. 269:15918-15924(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE-5619523; PubMeds627182; Weber W. Uguccioni M., Baggiolini M., Clark-Lewis I., Dahinden C.A.; Weber M., Uguccioni M., Baggiolini M., Clark-Lewis I., Dahinden C.A.; "Deletion of the NIZ-terminal residue converts monocyte chemotactic protein I from an activator of basophil mediator release to an eosinophil chemoattractant.";
                                                                                                                                                                                                                                                               MEDLINE=97143315; PubMed=898926;
Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;
"The structure of MCP-1 in two crystal forms provides a rare example of variable quaternary interactions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR.
MEDLINE=96234959; PubMed=8639605;
Handel T.M., Domaille P.J.;
"Heteronuclear (IH, 13C, 15N) NMR assignments and solution structure of the monocyte chemoattractant protein-1 (MCP-1) dimer.";
Blochemistry 35:6569-6584(1996).
                     MEDINE-91312872; PubMed-1857712; Gronenborn A.M., Clore G.M.; Gronenborn A.M., Clore G.M.; Modeling the three-dimensional structure of the monocyte chemo-attractant and activating protein MCAF/MCP-1 on the basis of the solution structure of interleukin-8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.; "Structural characterization of a monomeric chemokine: monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFFECT OF DELETION OF N-TERMINAL RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97053697; PubMed=8898111;
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EMBL, M30816; AAA36330.1; JOINED.
EMBL, M31625; AAA36330.1; JOINED.
EMBL, M24545; AAA18164.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Exp. Med. 183:681-685(1996).,
                                                                                                                                                                                                     Protein Eng. 4:263-269(1991).
3D-STRUCTURE MODELING
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A Studer C., Urfer R.,

Studer C., Urfer R.,

RT "Cloning and expression of rhesus monkey monocyte chemoattractant

RT protein..."

Studer C., Urfer R.,

"Cloning and expression of rhesus monkey monocytes and basephils

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Chemotactic factor that attracts monocytes and basephils

similarity).

-!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).

-!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).

-!- SUBUNIT: Belongs to the intercrine beta (chemokine CC) family.

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modified and this statement is not removed. Usage by and for commercial

cut send an email to license@isb-sib.ch).
                                                                               1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV 60
                                                                                                      24 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADDFKQKWV 83
                                                 Gaps
                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Carcopithecinae; Macaca.
Macaca mulatta (Shesus macaque).

Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Carcopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECTES=M.fascicularis,
Studer C., Urfer R.;
"Cloning and expression of cynomolgus monkey chemoattractant
        Length 99;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-1.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL, AP255343; AAP67756.1; -
EMBL, AP255343; AAP67756.1; -
HSSP; P13500; IDOX.
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR000807; Fractalkine.
InterPro; IPR008097; Fractalkine.
Pfam; PP0048; ILB; 1.
PRINTS; PR01721; FRACTALKINE.
SMART; SM0199; SCT; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
CYtokine; Chemotaxis; Signal; Inflammatory response; Pyrrolidone carboxylic acid.
SIGNAL
SIGNAL
CHAIN
24 SPANILARITY.
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SMALL INDUCIBLE CYTOKINE
    100.0%; Score 405; DB 1; 100.0%; Pred. No. 1.5e-40; iive 0; Mismatches 0;
                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=M.mulatta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                               24 QPDAINAPVTCCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                                                                                                                                                         1 QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neutrophils.
--- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=94183284; PubMed=7510962;
Hosang K., Knoke I., Klaudiny J., Wempe F., Wuttke W., Scheit K.H.;
"Porcine luteal cells express monocyte chemoattractant protein-1
(MCP-1): analysis by polymerase chain reaction and cDNA cloning.";
Biochem. Biophys. Res. Commun. 199:962-968(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain,
Zach O.R.F.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Chemotactic factor that attracts monocytes, but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                     ;
PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIA 433CB88C64EE7A4F CRC64;
                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                             1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z48479; CAA88370.1; -.
EMBL; X79416; CAA85945.1; -.
PIR; JC2136; JC2136.
HSSP; P13500; 1D0M.
InterPro; IPR0018911; Chēmokine_ILē.
InterPro; IPR0018911; Chēmokine_ILē.
Pfam; PP00046; ILē; 1.
PROSITIE; PR00472; SMALL, CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Sīgnal; Inflammatory response; Pyrrolidone carboxylic acid.
SIGMAL
24 SMALL; INDUCIBLE CYTOKINE ACID.
CYTOKINE; CHEMOTAXIE; SIGNAL, CYTOKINE ACID.
SIGMAL
24 SMALL; INDUCIBLE CYTOKINE ACID.
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SMALL INDUCIBLE CYTOKINE
                                                                                                                                                                                                          Score 394; DB 1;
Pred. No. 3e-39;
0; Mismatches
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75
37
11007 MW;
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ilarity 98.7%;
Conservative
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                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 74; Conserv
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                                                                                                                                           99 AA;
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TD SYO2 PIG
P42831;
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                                                                                                                                                                                                                                                                                      1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKIIVAKEICADPKOKWV 60
                                                                                                                                                                                                                                                                                                           24 QPDAIISPVTCCYTLINKKISIQRLASYKRVTSSKCPKBAVIFKTVLNKEICADPKQKWV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Seminal plasma;
MEDLINE-92181448; PubMed-1543494;
Nempe F., Einspanier R., Scheit K.H.;
"Characterization by cDNA cloning of the mRNA of a new growth factor farm bovine seminal plasma: acidic seminal fluid protein.";
Biochem. Biophys. Res. Commun. 183:232-237(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Seminal plasma;
MEDLINES-2096117, PubMed=1721821;
Wempe F., Henschen A., Scheit K.H.;
"Gene expression and cDNA cloning identified a major basic protein constituent of bovine seminal plasma as bovine monocyte-chemoattractant protein-1 (MCP-1).";
DNA Cell Biol. 10:671-679(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94338337; PubMed=8060303; Wempe F., Kuhlmann J.K., Scheit K.H.; "Characterization of the bovine monocyte chemoattractant protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Monocyte chemotactic protein 1A precursor (MCP-1A) (MCP-1) (Acidic seminal fluid protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Borine).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bowidae; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 202:1272-1279(1994).
- I- FUNCTION: Chemotactic factor that attracts monocytes, but not neutrophils.
                                                                                                                                                                                              Score 331; DB 1; Length 101;
                                        SMALL INDUCIBLE CYTOKINE A2. PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                      CDD7E2B1901A7267 CRC64;
                                                                                                                                                                                                                        7e-32;
                                                                                                       BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                           7; Mismatches
                       BY SIMILARITY
                                                                                       SIMILARITY)
                                                                                                                                                                                                                        Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                          84 ODSMAHLDKKSOTOTAK 100
                                                                                                                                                                                                                                                                                                                                                                             61 QDSMDHLDK--QTQTPK 75
                                                                                                                                                      101 AA; 11121 MW;
                                                                                                                                                                                                 81.7%;
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acid.
                                                                                                                                                                                                                                                62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
  Pyrrolidone carboxylic
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SEQUENCE FROM N.A.
                                            2 2
4 4
                                                                                                              34
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P28291;
                                                                                                            DISULFID
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                   Query Match
Best Local
                                                                 MOD_RES
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                     SIGNAL
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                                                                                                                                                                                                                                                                     83
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May play a significant role in monocyte trafficking into the reperfused myocardium.
SUBDNIT: Monomer or homodimer; in equilibrium (By similarity).
SUBCELULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Endothelium of small veins and intrafascicular veins, and infiltrating leukocytes.
INDUCTION: By INF-alpha leukocytes.
SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Jugular vein endothelial;

MEDLINES-9718620; PubMed-9024159;

Kumar A.G., Ballantyne C.M., Michael L.H., Kukielka G.L., Youker K.A.,
Lindsey M.L., Hawkins H.K., Birdsall H.H., Mackay C.R., Larosa G.J.,
Rossen R.D., Smith C.W., Entham M.L.,

"Induction of monocyte chemoattractant protein-1 in the small veins
of the ischemic and reperfused canine myocardium.";
                                                                                                                                                                                                                                                     24 QPDAINSPVTCCYTLTSKKISMQRLMSYRRVTSSKCPKEAVIFKTIAGKEICAEPKQKWV
                                                                                                                                                                                                                             1 OPDAINAPUTCCYNFINRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
115-MR-2004 (Rel. 43, Last annotation update)
Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Čhordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                   ..
       PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                      83.2%; Score 337; DB 1; Length 99; 80.0%; Pred. No. 1.4e-32; 2ive 8; Mismatches 7; Indels
                                                                                              4C0AC6278D4F0A09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1721; FRACTALKINE.
SMART; SMO0199; SCY, 1.
PROSITE; PSO00472; SMALL
CYTOKINE; Chemotaxis; SAIGNAI; Inflammatory response;
                         SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                           Pred. No. 1.46
8; Mismatches
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InterPro; IPR001811; Chemokine_IE8.
InterPro; IPR008097; Fractalkine.
Pfam; PF00048; IL8; 1.
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                                                                                              99 AA; 10976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Circulation 95:693-700 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U29653; AAA84911.1; -.
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein 1) (MCP-1) (M
CCL2 OR SCYA2 OR MCP1
                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
A EMBL; M84602; AAA30651.1;

PIR; A39296.

BR HSSP; P13500; 1DOM.

InterPro; 1PR000837; CC_chemkine_sml.

BR InterPro; 1PR000811; Chemokine_IL8.

BR SMATT; SM00199; SCT; 1.

BR PROSITE; P500472; SMALL CYTOKINES CC; 1.

KW Cytokine; Chemotaxie; Signal; Pyrrolidone carboxylic acid.

FT SIGNAL

24 99 MONOCYTE CHEMOTACTIC PROTEIN 1A.

25 BY SIMILARITY.

SIMILARITY.

SPROCLIDONE CARBOXYLIC ACID (BY SIMILARITY).

SPROCLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
protein 1) (MCP-1) (Monocyte chemoattractant protein-1)
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STRAIN=New Zealand white; TISSUE=Spleen;
MEDLINE=91225489; PubMed=2026877;
Yoshimura T., Yuhki N.;
"Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein-1 in rabbit. cDNA cloning and their chemoattractant protein-1 in rabbit. cDNA cloning and their J. Immunol. 146:3483-348 (1991).
-!- FUNCTION: Chemotactic factor that attracts monocytes, but not neutrophils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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InterPro; IPR001811; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
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84 QDSINYLNKKNQTPK 98
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SY02_RABIT
TO 2RABIT
AC P28232;
DT 01-DEC-1992
DT 01-DEC-1993
DT 01-DEC-
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MEDLINE-95034774; PubMed=7947749;

Prost P., Wayte A., Lenearts J.-P., van Damme J.;

Prost P., Wayte A., Lenearts J.-P., van Damme J.;

Pruffication, sequence analysis, and biological characterization of a second bovine monocyte chemotactic protein-1 (Bo MCP-1B).";

Blochemistry 33:13406-13412(1994).

Ascord bovine monocyte chemotactic factor that attracts monocytes, but not cherrophils. Augments monocyte anti-tumor activity. Also induces the release of gelatinase B. This protein can bind heparin.

C. -I- FUNCTION: Chemotactic factor that attracts monocytes, but not neutrophils. Augments monocyte anti-tumor activity. Also induces c.-I- FTM: The N-terminus is blocked.

C. -I- PTM: The N-terminus is blocked.

C. -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family. Hash: PROSSIP: DRO0049; ICB; I.

R. RESP: PISSOO 1807; CC Chemkine Sml.

R. REM: PROSO199; SCY: I.

R. SMART; SMO0199; SCY: I.

R. Cytokine; Chemotaxis; Heparin-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P01541)
10.1FB2-1995 (Rel. 31, Created)
01-FB2-1995 (Rel. 31, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Monocyte chemctactic protein 1B (MCP-1B) (Fragment).
Bos taurus (Bovine)
Extravpota Metacoa; Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidee;
SWART; SM00199; SCY; 1.

PROSITE; PS00412; SWALL CYTOKINES CC; 1.

PYCYCKINE; Chemotaxis; Signal; Inflammatory response; Glycoprotein;
Pyrrolidone carboxylic acid.

SIGNAL

I 23

SWALL INDUCIBLE CYTOKINE A2.

CHAIN

CHAIN

24

24

PYRROLIDONE CARBOXYLIC ACID (BY CYTOKINE A2.)

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PYRROLIDONE CARBOXYLIC ACID (BY CYTOKINE A2.)
                                                                                                   BY SIMILARITY.
SWALL INDUCIBLE CYTOKINE A2.
PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
M. 24C3A542CB6A47EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 77.5%; Score 314; DB 1; Length 125; Best Local Similarity 75.0%; Pred. No. 8.6e-30; Matches 57; Conservative 10; Mismatches 9; Indels
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BY SIMILARITY.
FAAF72B970EB16E3 CRC64;
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35 75 BY
40 40 N-1
55 55 N-1
112 112 N-1
125 AA; 13776 MW;
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10 50
74 AA; 8360 MW;
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ID MCPB BOVIN
AC P80343;
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84 ODFMKHLDKKTOTPK 98 Best Local Similarity 99 AA; [8] STRUCTURE BY NMR. 54; MOD RES DISULFID DISULFID HELIX SEQUENCE CONFLICT Query Match CARBOHYD STRAND SIGNAL STRAND STRAND Matches TURN WARANA HARARARANA WARANA W g ò g ò MEDLINE=9230885; PubMed=1613466; van Damme J., Prossiber G.; van Damme J., Prossi P., Lenaerts J.-P., Opdenakker G.; Structural and functional identification of two human, tumor-derived monocyte chemotactic proteins (MCP-2 and MCP-3) belonging to the SEQUENCE FROM N.A.
MEDLINE=93305913; PubMed=8318676;
Minry A., Chalon P., Guillemot J.C., Kaghad M., Liauzun P.,
Magazin M., Miloux B., Minty C., Ramond P., Vita N., Lupker J.,
Shire D., Ferrara P., Caput D.;
"Molecular cloning of the MCP-3 chemokine gene and regulation of its MEDLINE=97263733; PubMed=9109648; Meunler S., Bernara P., Darbon H.; Meunler S., Bernassau J.-M., Guillemot J.-C., Ferrara P., Darbon H.; "Determination of the three-dimensional structure of CC chemokine monocyte chemoattractant protein 3 by 1H two-dimensional NVR Opdenakker G., Fiten P., Nys G., Froyen G., van Roy N., Speleman F., of 01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Small inducible cytckine A7 precursor (CCL7) (Monocyte chemotactic
protein 3) (MCP-3) (Monocyte chemoattractant protein 3) (NC28).
CCL7 OR SCYA7 OR MCP3.
Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; SEQUENCE FROM N.A., AND SEQUENCE OF 31-67 AND 71-99.
MEDLINE=93213290; PubMed=8461011;
Opdenakker G., Froyen G., Fiten P., Proost P., van Damme J.;
Human moncyte chemotactic protein-3 (MCP-3): molecular cloning
the cDNA and comparison with other chemokines.";
Biochem. Biophys. Res. Commun. 191:535-542(1993). Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
"Structural characterization of a monomeric chemokine: monocyte
chemoattractant protein-3";
FEBS Lett. 395:277-282(1996). Laureys G., van Damme J.; cloning, sequence analysis, and assignment to the C-C chemokine gene cluster on chromosome SEQUENCE OF 24-99 FROM N.A. Jang J.S., Kim B.E.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. 99 AA Eur. Cytokine Netw. 4:99-110(1993) STRUCTURE BY NMR, AND SUBUNIT. MEDLINE=97053697; PubMed=8898111; SEQUENCE FROM N.A. MEDLINE=94375065; PubMed=7916328; spectroscopy."; Biochemistry 36:4412-4422(1997) chemokine family."; J. Exp. Med. 176:59-65(1992) STRUCTURE BY NMR.

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                                                                                                                                                                                                               -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: O-glycosylated.
-!- PTM: Similarity: Belongs to the intercrine beta (chemokine CC) family.
   Kwon D., Lee D., Sykes B.D., Kim K.-S.;
Submitted (AUG-1998) to the PDB data bank.
-!- FUNCTION: Chemotactic factor that attracts monocytes and
ecsinophils, but not neutrophils. Augments monocyte anti-tumor
activity, Also induces the release of gelatinase B. This protein
can bind heparin. Binds to CCR1, CCR2 and CCR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
T -> K (IN REF. 5).
MISSING (IN REF. 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMALL INDUCIBLE CYTOKINE A7. PYRROLIDONE CARBOXYLIC ACID.
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Lee D., Sykes B.D., Kim K.-S.;
1 (AUG-1998) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, X72308; CAA51055.1, ALT INIT.
EMBL, X72309; -, NOT ANNOTATED_CDS.
EMBL, X71087; CAA50406.1, ALT_INIT.
EMBL, X71087; CAA50406.1, ALT_INIT.
EMBL, X71087; CAA50406.1, ALT_INIT.
EMBL, AF043338; AAC03538.1; -, PDB; INCV, 15-OCT-97.
GDB, INCV, 10-OCT-97.
GDB, HDO0; 10-OCT-97.
MIM, 158106; -.
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Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Table Figure 1. Sequence polymorphisms in the chemokines Scyal (TCA-3), Scyal monocyte chemoattractant protein (MCP)-1), and Scyall (MCP-5) are candidates for each, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";

U. Immunol. 163:2262-2266(1999).

I. FUNCTION: Chemotactic factor that attracts eosinophils, monocytes, and lymphocytes but not neutrophils. Potent monocyte active chemokine that signals through CCR2. Involved in allergic chemokine. States and may play a pivotal role during early stages of allergic lung inflammation.

I. SUBCELLULAR LOCATION: Secreted.

I. SUBCELLULAR LOCATION: Secreted.

I. SUBCELLULAR LOCATION: Secreted.

I. SUBCELLULAR LOCATION: Secreted.

I. TISSUE SPECIFOTIY: Predominantly expressed in the lymph nodes, thymus. Also found in the salivary glands containing lymph nodes, breast, heart, lung, brain, small intestine, kidney and colon.

I. INDUCTION: By interferon gamma and lipopolysaccharides (LPS).

I. POLYMORPHISM: The polymorphism in strain SULJ, may be associated encephalomyelitis, an animal model of multiple sclerosis, and succephalomyelitis, an animal model of multiple sclerosis, and succephalomyelitis, an animal model of multiple sclerosis, and succephalomyelitis, an animal model of multiple sclerosis, and succephalomyelitish protein remitting/nonrelapsing form of the monophasic remitting/nonrelapsing form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97149438; PubMed=8996246; Sarafi M. Charo I.F., Luster A.D.; Sarafi M.N., Garcia-Cepeda B.A., McLean J.A., Charo I.F., Luster A.D.; "Murine monocyte chemoattractant protein (MCP)-5: a novel CC chemokine that is a structural and functional homologue of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                           SY12 MOUSE STANDARD; PRT; 104 AA.

062401; 090YD6;
01-N0V-1997 (Rel. 35, Created)
15-MAR-2004 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Small inducible cytokine Al2 precursor (CCI12) (Monocyte chemotactic proterin S) (MCP-5) (MCP-5) (MCP-7) (MCP-5) (MCP-6) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MADDLINE-97079149; PubMed=8920881; MADLINE-97079149; PubMed=8920881; MADDLINE-97079149; Martinez A.C., Jid G.G., Gonzalo J.A., Lloyd C., Kremer L., Lu L., Martinez A.C., Wershil B.K., Gutierrez-Ramos J.C.; Marshil B.K., Gutierrez-Ramos J.C.; Marshil B.K., Gutierrez-Ramos J.C.; Marshil B.K., Gutierrez-Ramos J.C.; J.C.; Marshil B.K., Gutierrez-Ramos J.C.; J. Exp. Med. 184:1939-1951(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=B10.S/J, BALB/C, DBA/ZJ, NOD/LTJ, and SJL/J; TISSUE=Spleen,
MEDLINE=99370037; Pubmed=10438970;
Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.;
Blankenhorn E.P.;
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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EMBL, U66670; AAB49424.1; -.
EMBL, AF065934; AAF15384.1; -.
EMBL, AF065935; AAF15385.1; -.
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                                                 R MBL, AF065940,

R HSSP; P13500; 1DOL.

DR MGD; MGI:108224; Ccl12.

DR InterPro; IPR000827; CC_chemkine_sml.

DR InterPro; IPR001811; Chemckine_IL8.

DR Pfam; PF00048; IL8; 1.

DR SYART; SM00199; SCY; 1.

DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.

CYLOKINE; Chemctaxis; Signal; Inflammatory response; Polymorphism.

**AMALL INDUCIBLE CYTOKINE A12.

**AMALL INDUCIBLE CYTOKINE A13.

**AMALL IND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-S6181789; PubMed-8597956;
Garcia-Zepeda E.A., Rothenberg M.E., Ownbey T.R., Leder P.,
Luster A.D.;
"Human ecravin is a specific chemoattractant for eosinophil cells and
provides a new mechanism to explain tissue eosinophilia.";
Nat. Med. 2:449-456(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 PDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKBICADPKQKWVQ
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PSIG71, FGSR77; Q92490; Q92491;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ectasin precursor (Small inducible cytokine All) (CCLII) (Eosinophil CCLII OR SCYAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDIATE=56189937; PubMed=8609214;
Ponath P.D., Qin S., Ringler D.J., Clark-Lewis I., Wang J., Kassam N. Smith H., Shi X., Gonzalo J.A., Newman W., Gutierrez-Ramos J.C.,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=96205964; PubMed=8631813;
Kitaurza M., Nakajima T., Imai T., Harada S., Combadiere C.,
Tiffany H.L., Murphy P.M., Yoshie O.;
"Molecular cloning of human ectaxin, an ecsinophil-selective CC chemckine, and identification of a specific ecsinophil ectaxin receptor, CC chemckine receptor 3.";
J. Biol. Chem. 271:7725-7730(1996).
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BD102F4FF4CG3DBF CRC64;
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68.1%; Pred. No. 2.3e-26;
tive 15; Mismatches 8; Indels
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34 74 BY
94 104 QT
104 AA; 11659 MW;
AF065936; AAF15386.1; -. AF065937; AAF15387.1; -. AF065938; AAF15388.1; -.
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les 49; Conservative
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84 NSINHLDKTSQT 95
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DISULFID
VARIANT
SEQUENCE
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SEQUENCE FROM N.A., SEQUENCE OF 60-65 AND 75-88, AND VARIANTS.

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Attachuser R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunzartne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length

Lorc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                        "Genomic organization, complete sequence, and chromosomal location of the gene for human ectaxin (SCYAll), an ecsinophil-specific CC \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99380469; PubMed=9712872;

Crump M.P., Rajarathnam K., Kim K.S., Clark-Lewis I., Sykes B.D.;

Crump M.P., Rajarathnam K., Kim K.S., Clark-Lewis I., Sykes B.D.;

Crump M.P., Rajarathnam K., Kim K.S.,

Solution structure of cotaxin, a chemokine that selectively recruits

eosinophils in allergic inflammation.";

J. Biol. Chem. 273:22471-22479(1998).

-!- FUNCTION: In response to the presence of allergens, this protein
directly promotes the accumulation of eosinophils, a prominent
feature of allergic inflammatory reactions. Binds to CCR3.

-!- SUBCELDULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUBE-Lung;
MEDLINE=97445071; PubMed=9299399;
Hein H., Schlueter C., Kulke R., Christophers E., Schroeder J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic organization, sequence, and transcriptional regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Delayed production of biologically active O-glycosylated forms of human ectaxin by tumor-necrosis-factor-alpha-stimulated dermal
                                                                                                                                                                                                                                                               Garcia-Zepeda E.A., Rothenberg M.E., Weremowicz S., Sarafi M.N., Morton C.C., Luster A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98237580; PubMed-9578468;
Noso N., Bartels J., Mallet A.I., Mochizuki M., Christophers E.
                                                      MEDLINE=96374440; PubMed=8780731;
Bartels J., Schlueter C., Richter E., Noso N., Kulke R.,
Christophers E., Schroeder J.-M.;
"Human dermal fibroblasts express ectaxin: molecular cloning,
expression, and identification of ectaxin sequence variants."
Biochem. Biophys. Res. Commun. 225:1045-1051(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the human ectaxin gene.";
Biochem. Biophys. Res. Commun. 237:537-542(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                            TISSUE=Placenta;
MEDLINE=97312708; PubMed=9169149;
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                         TISSUE-Foreskin;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
INDUCTION: By TNF-alpha, interleukin-1 alpha and interferon gamma. PTM: O-LINKED GIYCAN CONSIGNS OF A GAL-GALMAC DISACCHARIDE WHICH IS MOPIFIED WITH UP TO 2 SIALIC ACID RESIDUES.
SIMILARITY: Belongs to the intercrine beta (chemokine CC) family. DATABASE: NAME=R&D Systems' cytokine source book: SCYA11; WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=196".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.4%; Score 273; DB 1; Length 97; llarity 68.6%; Pred. No. 4.1e-25; Conservative 12; Mismatches 10; Indels
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FTIG=VAR 001634.

A -> T (IN CLONE 53).

FTIG=VAR 001635.

R -> S (IN CLONE 34).

FTIG=VAR 001636.

K -> R (IN CLONE 53).

FTIG=VAR 001637.
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L -> P (IN CLONE 34).
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VARIANT
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27 SVPTTCCFNLANRKIPLQRLESYRRITSGKCPQKAVIFKTKLAKDICADPKKKWVQDSMK 86
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FEBS Lett. 395:277-282(1996).
-! FWOTION: Chemotactic factor that attracts monocytes, lymphocytes, lymphocytes, chemotactic factor that attracts monocytes, lymphocytes, basophils and eosinophils. May play a role in neoplasia and inflammatory host responses. This protein can bind heparin.
-! STBUNIT: Monomer or homodimer; in equilibrium.
-! TISSUE SPECIFICITY: Highest expression found in the small intestine and peripheral blood cells. Intermediate levels seen in the heart, placenta, lung, skeletal muscle, thymus, colon, ovary, spinal cord and pencreas. Low levels seen in the brain, liver, spinal cord and pencreas. Low levels seen in the brain, liver, spinal cord.
-! INDUCTION: By interferon gamma, mitogens and interleukin-1.
-! SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECURNCE FROM N.A., AND VARIANT GLN-69.
MEDLINE=97237052; PubMed=9119400;
Van Coillie E., Fiten P., Momiyama H., Sakaki Y., Miura R., Yoshie O.,
Van Damme J., Opdenakker G.,
"The human MCP-2 gene (SCYA8): cloning, sequence analysis, tissue
expression, and assignment to the CC chemokine gene contig on
chromosome 17q11.2.";
Genomics 40:323-331(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Osteosarcoma;
MEDLINE-92308855; PubMed=1613466;
van Damme J., Proost P., Lenaerts J.-P., Opdenakker G.;
Vaructural and functional identification of two human, tumor-derived
monocyte chemotactic proteins (MCP-2 and MCP-3) belonging to the
chemokine family.";
                                                                                                                                                                                                                                      SY08 HUMAN STANDARD; PRT; 99 AA.

SY08 HUMAN STANDARD; PRT; 99 AA.

SR0075; P78388;
01-DEC-1992 (Rel. 24, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Small inducible cytokine A8 precursor (CCL8) (Wonocyte chemotactic protein 2) (MCP-2) (Monocyte chemoattractant protein 2) (HC14).

GCL8 OR SCYAB OR SCYAIO OR MCP2.

Homo sapiens (Human).
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MEDLINE=37224420; PubMed=9070881;
MEDLINE=37224420; PubMed=9070881;
MEDLINE=37224420; Proyen F., Nomiyama H., Miura R., Fiten P.,
van Aelst I., van Damme J., Opdenakker G.;
Hunan moncoyte chemceactic protein-2: cDNA cloning and regulated
expression of mRNA in mesenchymal cells.";
Biochem. Biophys. Res. Commun. 231:726-730(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 23-99 FROM N.A.
MEDLINE=91207938; PubMed=2518726;
Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;
"Cloning and expression of a gamma-interferon-inducible gene in monocytes: a new member of a cytokine gene family.";
Int. Immunol. 1:388-399(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97053697; PubMed=8898111;
Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
"Structural characterization of a monomeric chemokine: monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANT GLN-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemokine family.";
J. Exp. Med. 176:59-65(1992).
                                                      66 HLDKQTQTPK 75
|||::||:
87 YLDQKSPTPK 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
Polymorphism; Pyrrolidone carboxylic acid; 3D-structure.
SIGNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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MEDLINE-95091716; PubMed=7999015;
Medline-95091716; PubMed=7999015;
Medline-95091716; Muttke W.W.,
Scheit K.K.;
Porcine luteal cells express monocyte chemoattractant protein-2
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66.2%; Score 268; DB 1; Length 99
Best Local Similarity 62.7%; Pred. No. 1.6e-24;
Matches 47; Conservative 13; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-07T-1996 (Rel. 34, Created)
01-07T-1996 (Rel. 34, Last sequence update)
10-07T-2003 (Rel. 42, Last annotation update)
small inducible cytokine A8 precursor (CCL8) (Monocyte ck
protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
CCL8 OR SCYAR OR MCP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMALL INDUCIBLE CYTOKINE AB.
PYRROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
K -> Q.
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9D67976BB9422F2A CRC64;
                                                                                                                                                                                                                                                                                                                                            MIM, 602283; -. GO 60008019; F:chemokine activity; TAS. GO; GO:0008019; F:signal transducer activity; TAS. GO; GO:000811; F:signal transducer activity; TAS. GO; GO:0006815; P:calcium ion transport; TAS. GO; GO:0006395; P:chemotaxis; TAS. GO; GO:0006887; P:excoytosis; TAS. GO; GO:0006817; P:excoytosis; TAS. GO; GO:0006415; P:response to viruses; TAS. GO; GO:0007165; P:response to viruses; TAS. GO; GO:0007165; P:response to viruses; TAS. InterPro; IPRO00827; CC_chemkine_sml.
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                                                                                                                                                                        EMBL; X99886; CAA68168.1; ALT_INIT.
EMBL; X10802; CAA71760.1; --
EMBL; X16645; CAA76341.1; --
PLR; Y05295; JG5295.
PDB; 1ESR; 06-DEC-00.
Genew; HGNC:10635; CCL8.
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SY08 PIG
ID SY08 PIG
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DISULFID
DISULFID
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07330446.pep.rsp

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SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.
                                                                                                                                                                                                    Exp. Med. 183:2379-2384(1996).
                                                                 MEDLINE=96235049; PubMed=8642349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gray P.W.;
              REFFERER REFERER REFERER REFFERER REFFE
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(MCP-2): analysis by cDNA cloning and northern analysis.";
Biochem. Biophys. Res. Commun. 205:148-153(1994).
-!- FUNCTION: Chemotactic factor that attracts monocytes. This protein can bind heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 OPDAINAPVICCYNFINRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 QPDSVSIPITCCFGLVNGKIPFKKLESYTRIINSQCPQBAVIFKTKADKEVCADPQQKWV
                                                                                                            -!- SUBUNIT: Monomer or homodimer, in equilibrium (By similarity).
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMARI; SHUULDS; SUL; 1.
PROSITE; PSO0472; SMALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last sequence update)
Small inducible cytokine All precursor (CCL13) (Monocyte chemotactic process 4) (MCP-4) (Monocyte chemoattractant protein 4) (MCP-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
SMALL INDUCIBLE CYTOKINE A8.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.4%; Score 261; DB 1; Length 99; 60.0%; Pred. No. 1.1e-23; ive 16; Mismatches 14; Indels
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BY SIMILARITY.
BY SIMILARITY.
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InterPro; 1PR000837; CC chemkine sml.
InterPro; 1PR001811; Chemokine_IL8.
Pfam; PF00048; 1L8; 1.
SMART; SM00199; SCY; 1.
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MEDLINE=97113354; PubMed=8955214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCL13 OR SCYA13 OR MCP4 OR NCC1. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z48480; CAA88371.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 AA; 10903 MW;
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Les 45; Conserv
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SIGNAL CHAIN

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NEDLINE=22388257; PubMed=12477932;

RETAINE=22388257; PubMed=12477932;

RIAURE=22388257; PubMed=12477932;

RIAURE=22388257; PubMed=12477932;

RIAURE R.D., Collins F.S., Magner L., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemer C.F., Bhat N.K.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA HOpkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Branchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raplecon M., Scares M.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,

Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaranne P.H.,

Robak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaranne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Soderson M.A., Rodrigues S., Sanchez A.,

Raha S., Morley K.C., Shevohenko Y., Bouffard G.G.,

Rahay J., Helton E., Woung A.C., Shevohenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schwutz J., Myrrs R.M.,

Raha Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E.,

Robert A., Maran and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Uguccioni M., Loetscher P., Forssmann U., Dewald B., Li H., Lima S.H., Li, X Kraider B., Garotta G., Thelen M., Baggiolini M.; "Monocyte chemotactic protein 4 (MCP-4), a novel structural and functional analogue of MCP-3 and ectaxin.",
                                                                                                                                                                                                                                                                                                                                                                                        MEDIJUE=97341179; PubMed=9195948;
MEDIJUE=97341179; PubMed=9195948;
MEDIJUE=97341179; PubMed=9195948;
Machine E., Reape T.J., Brawner M., Makwana J., Foley J.J.,
Schmidt D.B., Imburgia C., Machulty D., Matthews J., O'Donnell K.,
O'Shannessy D., Scott M., Groot P.H.E., Macphee C.,
"Cloning, in vitro expression, and functional characterization of a novel human CC chemokine of the monocyte chemocactic protein (MCP) family (WCP-4) that binds and signals through the CC chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=97213770; PubMed=9060459;
Godiska R., Chantry D., Raport C.J., Schweickart V.L., Trong H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic organization, sequence analysis and transcriptional regulation of the human MCD-4 chemokine gene (SCYA13) in dermal fibroblasts: a comparison to other eosinophilic beta-chemokines."; Biochem. Biophys. Res. Commun. 255:470-476(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Skin fibroblast;
MEDLINE=99160888; PubMed=10049733;
Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,
Bartels J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Monocyte chemotactic protein-4: tissue-specific expression and signaling through CC chemokine receptor-2."; J. Leukoc. Biol. 61:353-360(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dante M., Gibson A.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor 2B.";
J. Biol. Chem. 272:16404-16413(1997).
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                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: Widely expressed. Found in small intestine, thymus, colon, lung, trachea, stomach and lymph node. Low levels seen in the pulmonary artery smocth muscle cells.

INDUCTION: By interlevin-1 and TNP-alpha.

PTM: ONE MAJOR ISOFORM MCP-4, AND TWO MINOR ISOFORMS (IA) MCP-4 AND FFRENDITAL SIGNAL CLEAVAGE.

(LA) MCP-4 ARE PRODUCED BY DIFFRENDITAL SIGNAL CLEAVAGE.

(LA) MCP-4 IN THE PRODUCED BY DIFFRENDITAL SIGNAL CLEAVAGE.

MASS SPECTROMETRY: MW-9314; MW ERR=30; METHOD-MALDI; RANGE=17-98.

MASS SPECTROMETRY: WW-8576; MW ERR=30; METHOD-MALDI; RANGE=22-98.

MISCELLANBOUS: This protein can bind heparin.

SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                    Partels J.H., Schlueter C., Richter E., Noso N., Christophers E., Schroeder J.-M.; Achlueter C., Richter E., Noso N., Christophers E., Schroeder J.-M.; Achlueter C., Richter Barkers and F. Freezession of a MCP-4 like novel CC-chemokine in human dermal fibroblasts: molecular cloning and RT-PCR analysis."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: Chemoteatic factor that attracts monocytes, lymphocytes, basophils and eosinophils, but not neutrophils. Signals through CCR2B and CCR3 receptors. Plays a role in the accumulation of Leukocytes at both sides of allergic and nonallergic inflammation. May be involved in the recruitment of monocytes into the arterial wall during the disease process of artherosclarosis. May play a role in the monocyte attraction in tissues chronically exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMALL INDUCIBLE CYTOKINE A13, LONG FOR SMALL INDUCIBLE CYTOKINE A13, SHORT FC PYROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLOCNAC. . ) (POTENTIAL).
AMTIKT -> LIP (IN REF. 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1721; FRACTALKINE.
SMART; SMO0199; SCY; 1.
SMOSITE; PSO0472; SMALL_CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Signal; Glycoprotein; Inflammatory response;
Pyrrolidone carboxylic acid.
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0008009; F:chemokine activity; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0005102; F:receptor binding; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0006935; P:chemokrats; TAS.
GO; GO:0006935; P:chemokrats; TAS.
GO; GO:0006935; P:inflammatory response; TAS.
GO; GO:0006935; P:inflammatory response; TAS.
GO; GO:0006935; P:inflammatory response; TAS.
GO; GO:0007165; P:inflammatory response; TAS.
InterPro; IPR001811; Chemokine Ins.
InterPro; IPR001811; Chemokine Ins.
                                                                                                                                                                                                                                                                                                                                           exogenous pathogens.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC002482; AAB67307.1; -.
X98306; CAA66950.1; -.
U59808; AAD09362.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ001634; CAA04888 1; -.
EMBL; BC008621.1; -.
EMBL; Z77550; CAB01111.1; -.
HSSP; P51671; 1ECT.
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SEQUENCE OF 17-95 FROM N.A.
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CONFLICT
SEQUENCE
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MEDLINE=91293127; PubMed=2065676;

MEDLINE=91293127; PubMed=2065676;

Van Darme J., Decock B., Mantcovani A.;

Put W., Opdenakker G., Mantcovani A.;

Production and identification of natural monocyte chemotactic protein from virally infected murine fibroblasts. Relationship with product of the mouse competence (JE) gene.";

Bur. J. Blochem. 199:223-229(1991).

-!- FINGTION: Chemotactic factor that attracts monocytes, but not neutrophils.

-!- SUBRINIT: Monomer or homodimer; in equilibrium (By similarity).

-!- SUBRINIT: Monomer or homodimer; in equilibrium (By similarity).

-!- SUBRINIT: Monomer or homodimer; in strain SJL/J may be associated with severity of clinical symptoms of experimental allergic with severity of clinical symptoms of experimental allergic susceptibility to the monophasic remitting/nonrelapsing form of the disease.
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                                                                                                                                                                               24 QPDALNVPSTCCFTFSSKKISLQRLKSY-VITTSRCPQKAVIFRTKLGKEICADFKEKWV
                                                                                                                                         1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV
                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P10148, Q9QVD7;
01-WAR-1989 (Rel. 10, Created)
01-WAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last sanotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1) (Platelet-cCL2 OR SCYA2 OR MCP1 OR JE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS GLY-50 AND GLN-92. STRAIN=B10.S/J, BALB/c, DBA/2J, NOD/LTJ, and SJL/J; TISSUE=Spleen; MSDLINE=99370037; PubMed=10438970; Tenscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W., Blankenhorn E.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawahara R.S., Deuel T.F., "Plactor-inducible gene JE is a member of "Platelet-derived growth factor-inducible gene JE is a member of family of small inducible genes related to platelet factor 4."; J. Biol. Chem. 264:679-682(1989).
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                                                                    Indels
62.6%; Score 253.5; DB 1
60.5%; Pred. No. 7.8e-23;
ive 16; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                    83 QNYMKHLGRKAHTLKT
Query Match
Best Local Similarity 60.5°
Matches 46; Conservative
                                                                                                                                                                                                                                                                                          61 QDSMDHLDKQTQTPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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DISULFID
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                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota, Metazos, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.2%; Score 252; DB 1; Length 148; 60.9%; Pred. No. 1.8e-22; ive 17; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P13500; 1DOK.

MGD; MGI:99259; Cc12.

MGD; MGI:0901664; F:G-protein-coupled receptor binding; IDA.

GO; GO:0001664; F:protein binding; IDA.

InterPro; IPR000827; CC_chemkine_sml.

InterPro; IPR001811; Chemokine_ID8.
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MEDLINE=94114084; PubMed=8286035;
Wempe F., Hanes J., Scheit K.H.;
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EMBL, AF065931; AAF15380.1; --
EMBL, AF065931; AAF15381.1; --
EMBL, AF065932; AAF15382.1; --
EMBL, AF065932; AAF15383.1; --
PIR; A30209; A30209.
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EMBL; M19681; AAA37684.1; -.
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Matches 42; Conservative
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84 QTYIKNLDR 92
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Q09141;
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can bind hearing.

-1 - SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).

-1 - SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).

-1 - SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.

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"Cloning of the gene for bovine monocyte chemoattractant protein-2."; DNA Cell Biol. 13:1-8(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S67954; AAD14005.1; --
EMBL; S67956; AAB29750.1; --
EMBL; S67956; AAB29750.1; --
EMBL; S67956; AAB29750.1; --
HSSP; S1671; LEOT.
InterPro; IPR010811; Chēmokine_IE8.
InterPro; IPR011811; Chēmokine_IE8.
SNART; SM00139; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
CYLOKINE; Chemotaxis; Signal; Hepaxin-binding; Inflammatory response;
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SMALL INDUCIBLE CYTOKINE A8.
PYRROLIDONE CARBOXYLIC ACID
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01974CDB3FF9119B CRC64;
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35 75
99 AA; 10900 MW;
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Best Local Similarity
Matches 42; Conserv
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Ogttg3 equus cabal		Q8mkc8 equus cabal	Q865f4 macaca neme	Q8hyq0 macaca mula	QBmit7 macaca mula	Q8hxz5 macaca mula	Q8cgm5 sigmodon hi	Q9ttg4 equus cabal	Q9z318 cavia porce	Q95md5 bos taurus	Ostts6 bos taurus	Ogttq2 equus cabal		
SUMMARIES	Q9TTQ3	Q7Z7Q8	Q8MKC8	Q865F4	08HXO0	Q8MIT7	Q8HXZ5	QBCGMS	Q9TTQ4	092318	Q95MD5	Q9TTS6	Q9TTQ2	QSTTQ1	092690
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ALIGNMENTS

Length 99;

DB 6;

81.5%; Score 330;

Query Match

0; Gaps

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1 QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
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assignment to the C-C chemokine gene cluster on chromosome 17q11.2-
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 72.0%; Pred. No. 6.4e-28;
Matches 54; Conservative 4; Mismatches 17; Indels
                                                                                        Ğenonics 21:403-408(1994).
EMBL; X72309; CAB59723.1; -.
SEQUENCE 109 AA; 12356 MW; 69980669F0A2157D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 AA
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GO, GO:0005576; C:extracellular; IEA.
GO, GO:0008009; F:chemckine activity; IEA.
GO; GO:0008055; P:chemckine activity; IEA.
GO; GO:0006955; P:lmmune response; IEA.
Pfam; PF00048; ILB: 1.
SMART; SM00199; SCY: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBMKC8
QBMKC8;
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Q865F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
QSMKC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 QPDGINTSTTCCYRFINKKIPKQRLESYRRITSSHCPREAVIFKTKLDKEICADPTQKWV 93
                                                                                                                                         1 OPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV 60
                                                                                                                                                                                                                        83
                                                                                                                                                                                         24 QPDAINSPVTCCYTFTGKKISSQRLGSYKRVTSSKCPKBAVIFKTILAKEICADPEQKWV
                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEGUENCE FROM N.A.

Coleman G.D., Valli P.J.S., Clements J.E., Zink M.C.;

Macaca nemestrina (Pig-tailed macaque) monocyte chemoattractant

"Macaca nemestrina" (Pig-tailed macaque) monocyte chemoattractant

"Macaca nemestrina" (MCP-3).";

E.M. MCP-3).";

E.M. MCP-3).";

E.M. MGC-2002)' to the EMBL/GenBank/DDBJ databases.

E.M. MGC-20005576; C:extracallular; IEA.

GO; GO:0005576; C:extracallular; IEA.

GO; GO:0005576; C:extracallular; IEA.

GO; GO:0005576; C:extracallular; IEA.

RO; GO:0005576; C:extracallular; IEA.

RO; GO:0005676; C:extracallular; IEA.

RO; GO:000695; P:chemokine activity; IEA.

RO; GO:000695; P:chemokine activity; IEA.

RO; GO:000695; P:chemokine IIA.

RO; GO:000695; P:chemokine IIA.

RO; GO:000695; P:manne response; IEA.

RO; GO:000695; P:manne response; IEA.

RO; GO:000695; P:manne response; IEA.

RO; GO:000695; P:chemokine IIA.

RO; GO:000695; P:manne response; IEA.

RO; GO:000695; P:manne response; IEA.

RO; GO:000695; P:chemokine IIA.

RO; GO:000695; P:chemokine IIA.

RO; GO:000695; P:manne response; IEA.

RO; GO:000695; P:chemokine IIA.

RO; GO:0006969; P:chemokine IIA.

RO; GO:00069; P:chemokine IIA.

RO; GO:000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDINE=9437665; PubMed=7916328;
Opdenakker G.M.M.;
"The human MCP-3 gene (SCYA7): cloning, sequence analysis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .Match 73.3%; Score 297; DB 6; Length 109; Local Similarity 73.3%; Pred. No. 3.6e-29; les 55; Conservative 5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca nemestrina (Pig-tailed macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                      78.7%; Pred. No. 2.5e-33; ative 9; Mismatches 7; Indels
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(TremBlrel. 25, Last sequence update)
(TremBlrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monocyte chemoattractant protein-3.
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84 QDAVKQLDKKAQTPK 98
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                                                                                                                                                                                                                                                                                                            61 QDSMDHLDKQTQTPK 75
                                                                  59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                      Best Local Similarity
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01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                               SEGUENCE FROM N.A.
Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
"Equus caballus monocyte chemoattractant protein-2 (mcp-2), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN 2003 (TrEMBLrel, 24, Created)
01-JUN-2003 (TrEMBLrel, 24, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last sequence update)
Monocyte chemoattractant protein-2.
Macaca nemestrina (Pig-tailed macaque).
Macaca nemestrina (Pig-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
[1]
                                                                                                                                                      Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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0
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                                                                                                                                                                                                                                                                                                                                                                                    cds.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 AA; 11028 MW; 94F5D8E540889228 CRC64;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                      RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKBAVIFKTIVAKEICADPKQKWV
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P SEQUENCE FROM N.A.

A Coleman G.D., Clements J.E., Zink M.C.;

Macaca nemestrina (pig-tailed macague) MCP-2 (CC) chemokine.";

L. Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

R. Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

R. RASI, AY206693, AA052734.1;

R. GO; GO:0016576; C:extracellular; IEA.

R. GO; GO:0016576; C:emembrane; IEA.

R. GO; GO:001655; P:chemokine activity; IEA.

R. GO; GO:0008099; P:chemokine sml.

R. InterPro; IPR001811; Chemokine sml.

R. InterPro; IPR001811; Chemokine ILB.

R. InterPro; IPR001817; Fractalkine.

R. Program, PR00148; IEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ChemoKine CCL8/MOP-2.
Macaca mulatta (Rhesus macaque).
Macaca milatta (Rhesus formata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A., "Comprehensive cloning and sequencing reveals evolutionary conservation among all groups of rhesus macaque chemokines.", Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.9%; Score 271; DB 6; Length 99; 62.7%; Pred. No. 5.7e-26; ive 14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.7%; Score 274; DB 6; Length 99, 62.7%; Pred. No. 2.46-26; cive 14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, #444289; AAN76073.1; -
GO; GO:000575; C:extracellular; IEA.
GO; GO:000502; C:membrane; IEA.
GO; GO:000809; F:chemokine activity; IEA.
GO; GO:0008095; F:chemokine response; IEA.
INTERPRO; IPRO0827; CC Chemkine sml.
INTERPRO; IPRO08097; Practalkine.
INTERPRO; PRO08097; Practalkine.
PRINTS; PRO1721; FRACTALKINE.
SMART; SM00199; SCY; I.
SMART; SM00199; SCY; I.
SMART; SM00199; SCY; I.
SSQUENCE 99 AA; 11263 MW; 9D6797974A88BF7F CRC64;
                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1721; FRACTALKINE.
SMART; SMOOL99; SCY; 1.
PROSTIE: PSO0472; SMALL CYTOKINES CC; 1.
SEQUENCE 99 AA; 11281 MW; 9D6797974A88B9BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 62.7%,
Local 47; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 Орѕмригркототрк 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 RDSMKHLDQMFQNLK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QDSMDHLDKQTQTPK 75
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47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
08HYQ0
10 MHYQ0
DT 01-M
DT 01
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2 PDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKBAVIFKTIVAKEICADPKQKWVQ 61
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
chemokine CCL11/cotaxin.
Macaca mulatta (Rhesus macaque).
Macaca mulatta (Rhesus macaque).
Mammalia, Eutheria, Primates; Carariata, Vertebrata, Euteleostomi, Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
"Comprehensive cloning and sequencing reveals evolutionary
conservation among all groups of Fresus macaque chemokines.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF449270; AAN76074.1; -.
GO; GO:0005576; C:sxtracellular; IEA.
GO; GO:0005576; C:sxtracellular; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                        Zhang L., Soares M.P., Guan Y., Sirotina-Meisher A.,
Matheravidathu S., Iliff S.A., Mudgett J.S., Springer M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                  01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.4%; Score 261; DB 6; 63.5%; Pred. No. 9.8e-25;
                                                                                                     97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                     PRT;
                                                                                                                                                                                                  Macaca mulatta (Rhesus macaque)
62 DSMDHLDKQTQTPK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                вз рамкугряксетек 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 63.5
nes 47; Conservative
                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Daugherty B.L.;
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InterPro

83

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QBCGM5

RESULT 9

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1 OPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKBAVIFKTIVAKBICADPKOKWV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Lung;
Asano K., Makamura M., Oguma T., Fukunaga K., Matsubara H.,
Ishizaka A., Vamaguchi K., Kanazawa M.;
Ishizaka A., Vamaguchi K., Kanazawa M.;
Ishiferential expression of CC chemokines in guinea pig lungs during
an allergic inflammation.";
Submitted (MAY1-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ABA140; BAA36456.1;
HSSP; P51671; IEOT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monocyte chemoattractant protein-3 (MCP-3).
Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                   / Match 62.2%; Score 252; DB 6; Length 100; Local Similarity 64.0%; Pred. No. 1.3e-23; les 48; Conservative 13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN 24 100 EOTAXIN.
SEQUENCE 100 AA, 11247 MW, 11F08EC00E75D50B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 AA.
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GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC_chemkine sml.
InterPro; IPR01811; Chemokine_IE8.
Pfam; PF00048; ILB; 1.
                                                                                                                                                                                                                                                                                                                                                                                         GO, GO:0005576; C:extracellular; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR001811; Chemokine IEA.
InterPro; IPR008097; Fractalkine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFam; PF00048; ILB; 1.
PRINTS; PR01721; FRACTALKINE.
SMART; SM00199; SCY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QDSMDHLDKQTQTPK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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100
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                                                                                            SEQUENCE FROM N.A.
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                                      NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                         2 PDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKQKWVQ 61
                                                                                                                                                                                                                                                                                                                                                                                25 PDSV--ATTCCFTLTNKKIPLQRLESYRRIISGKCPQKAVIFKTKLAKDICADPKKKWVQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 OPDAINAPVICCYNFINRKISVORLASYRRITSSKCPKBAVIFKTIVAKBICADPKQKWV
                                                                                                                                                                                                                                                                                      2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signodon hispidus (Hispid cotton rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Planco J.C., Pletneva L.M., Prince G.A.;
Blanco J.C., Pletneva L.M., Prince G.A.;
"Sigmodon hispidus cytokines, chemokines and interferons.";
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
In EMBL, A71659531 AAN85636.1;
R GO, GO:0005576; C:extracellular; IEA.
GO; GO:0005557 P:immune response; IEA.
R GO; GO:0006555; P:immune response; IEA.
R InterPro; IPR000827; CC-chemkine sml.
InterPro; IPR001811; Chemokine_IIA.
R InterPro; IPR001811; Chemokine_IIA.
R SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.2%; Score 260; DB 11; Length 150; 63.2%; Pred. No. 2.1e-24; tive 11; Mismatches 17; Indels (
                                                                                                                                                                                                                         Query Match 64.4%; Score 261; DB 6; Length 97; Best Local Similarity 63.5%; Pred. No. 9.8e-25; Matches 47; Conservative 14; Mismatches 11; Indels
                                                                   Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 97 AA; 10795 MW; ED0CD482880A47C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 AA.
                   InterPro; IPR000827; CC_chemkine_sml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last seq 01-0CT-2003 (TrEMBLrel. 25, Last ann Monocyte chemoattractant protein-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                   IPR001811; Chemokine_IL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 OMYTKKMDONKARSET 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ООВМОНГОКОТОТРКТ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 DSMDHLDKQTQTPK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| :||::: |||
DSMKYLDRKSPTPK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=42415;
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Sigmodon

SO DRA RET RANK SO OCC SO DE TENTE RET RANK SO OCC SO OCC

SMART; SM00199; SCY; 1. PROSITE; PS00472; SMALL CYTOKINES CC; 1. SEQUENCE 97 AA; 11159 MW; E1B9A17C165C2421 CRC64;

Ectaxin precursor. Equus caballus (Horse). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Q9TTQ4 Q9TTQ4;

RESULT 10

Matches

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Gaps

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Vogel B., Klinder A., Aust G.;
"Molecular cloning of bovine ectaxin mRNN.";
submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132003. CAB6[617.1;
HSSP; P51671; IEOT.
GO, GO.0005576; C:extracellular; IEA.
GO, GO.0006595; F:chemokine activity; IEA.
GO, GO:0006955; P:immune response; IEA.
InterPro; IPR001811; Chemokine_IL8.
Fram; PF0018911; Chemokine_IL8.
Fram; PF001891; CX; 1.
SWART; SMO0199; SCY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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              S PRE BREEFE
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                                                                                                                                                                              1 OPDAINAPUTCCYNFTNRKISVORLASYRRITSSKCPKBAVIFKTIVAKEICADPKOKWV 60
                                                                                                                                                                                                                                           81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 QPDSVSTPITCCFSVINGKIPFKKLDSYTRIINSQCPQEAVIFKIKADRDVCADPKQKWV 84
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Chemoattractant protein 2 (Fragment).
Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla; Ruminantia; Pecora, Bovoidea;
NORI_TAXID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Werling D.;
"Role of chemokines in respiratory syncytial virus infection.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF399641; AAK94451.1; -.
HSSP; Q9Y258; 1G2S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.0%; Score 247; DB 6; Length 10
56.0%; Pred. No. 5.6e-23;
iive 19; Mismatches 14; Indels
                                                                                                              13; Indels
                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 AA; 11001 MW; F1D308AD924FCAF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.5%; Score 249; DB 11; 63.2%; Pred. No. 3.1e-23; ive 13; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:00080095; P:immune response; IEA.
InterPro; IPR001817; Cc. chemkine sml.
InterPro; IPR001811; Chemokine_II&.
Ffan, FP00484; ILB; I.
FR001FE; PS00472; SCY; I.
FROSITE; PS00472; SWALL_CYTOKINES_CC; I.
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82 QDSMKYIDKKSKTPKS 97
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                                          Query Match
Best Local Similarity 63.2<sup>1</sup>
Matches 48; Conservative
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hes 42; Conserv
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SEQUENCE FROM N.A.
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Q9TTS6
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O95MD5
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                                                                                                                          24 QPASI--PTICCFNMSKKKISIQRLQSYRKITSSKCPQKAVIFNTKQNKKICVDPQEKWV
                                                                                              1 OPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
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                                                   Gaps
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X MEDLINE-21061912; PubMed=11044560;

A Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,

A Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,

Collins M.E.;

"Cloning of equine chemokines eotaxin, monocyte chemoattractant proctein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and rinduction by IL-4 in dermal fibroblasts.";

I Vet. Immunol. Immunopathol. 76:283-298(2000).

R HSSP, P135000, 1DCK.

R GO; GO:00005956; C:extracellular; IEA.

GO; GO:0006955 p:immune response; IEA.

R GO; GO:0006955 p:immune response; IEA.

R DITEPPO; IPRO01811; Chemokine_ILB.

R Pfam; PF00048; ILB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equus caballus (Horse).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                   .,
58.0%; Score 235; DB 6; Length 97
55.3%; Pred. No. 1.7e-21;
ive 20; Mismatches 12; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Monocyte chemoattractant protein-2 precursor (Fragment).
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Pred. No. 1.4e-18;
9; Mismatches 11;
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     Query Match
Best Local Similarity 55.34
Matches 42; Conservative
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es 38; Conserv
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81
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SEQUENCE
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Length 97;

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| 1] | SEQUENCE FROM N.A. | Bamblan A.S., Horohov D.W., BEDLINE-21061912; PubMed=11044560; BEDLINE-21061912; PubMed=11044560; BEDLINE-21061912; PubMed=11044560; Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W., Collins M.E., | Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eguus caballus (Horse).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia, Eutheria, Perissodactyla, Equidae; Equus.
NCBI_TaxID=9796;
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O9TTQ1

D O9TTQ1

D O9TTQ1

D O9TTQ1

D O1TQ1

D O1TQ1

D O1TQ2

D O1-MAY-2000 (TrEMBLrel. 13, Created)

D O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

D O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

D O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

D O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)

D Moncoyte (hemoattractant protein-4 precursor (Fragment).

D Eduas caballus (Horse).

C Eduaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost occ Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OC MCBI_TaxID=9796;

RN [1]

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RA Benarafa C., Cunningham F.M., Hambin A.S., Horohov D.W., RA Benarafa C., Cunningham F.M., Hambin A.S., Horohov D.W., RA Benarafa C., Cunningham F.M., Hambin A.S., Horohov D.W., RA Colins M.E.;

RT Cloning of equine chemokines cotaxin, monocyte chemoattracts protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues induction by IL-4 in dermal fibroblasts.";

Not. Immunol. Immunopathol. 76:283-298(2000).

DR GO; GO:0008009; F:chemokine activity; IBA.

DR GO; GO:000809; F:chemokine activity; IBA.

CHAIN FFT SMO0199; SCY; 1.

FFT SIGNAL AND TER CHAIN

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SWART; SMO0199; ACY; 1.

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Search completed: August 30, 2004, 17:07:19 Job time : 119 secs

Best Local Similarity 58.6 Matches 34; Conservative

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1; Gaps

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 30, 2004, 16:49:12; Search t (without 7114.623	time 1389 Seconds t alignments) Million cell updates/sec
Title: Perfect score: 228 Sequence: 1 cagccagatgcaatcaatgcåa	.aaacccaaactccgaagact 228
Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	
Searched: 3470272 segs, 21671516995 residues	
Total number of hits satisfying chosen parameters:	6940544
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	,
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : GenEmbl:* 1: 90 ba:* 2: 95 in:* 4: 90 ou:* 5: 95 pa:* 6: 95 pa:* 10: 95 pa:* 11: 95 pa:* 11: 95 pa:* 12: 95 pa:* 13: 95 un:* 14: 95 un:* 14: 95 un:* 15: em ba:* 16: em fun:* 17: em in:* 18: em in:* 19: em ou:* 22: em ou:* 23: em pa:* 24: em pa:* 25: em pa:* 26: em in:* 27: em pa:* 28: em in:* 29: em un:* 29: em un:* 29: em htg inu:* 30: em htg inu:* 31: em htg inu:* 32: em htg inu:* 33: em htg inu:* 34: em htg inu:* 35: em htg inu:* 36: em htg inu:* 36: em htg inu:* 37: em htg inu:* 38: em htg inu:* 38: em htg inu:* 39: em htg inu:* 38: em htg inu:* 48: em htg inu:*	
	by chance to have a

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Gaps

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Indels

Length 228;

9 9 120 120 180 180

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Chases 1 to 300)

E 1 (bases 1 to 300)

E gashira, K., Takeshita, A., Koyanagi, M., Nakamuta, M. and Nishida, K. Noval hepatic disease agent

D Patent: WO 2030464-A.2 18-APR-2002; M., NAKIRA TAKESHITA, MASAMICHI KOYANAGI MAKOTO NAKAMUTA, KENICHI NISHIDA

OS Homo sapiens (human)

PD 18-APR-2002

PP 28-EBP-2001 WO 2001JP008552

PR 11-0CT-2000 UP 00P 310664

PI KENUKE EGASHIRA, AKIRA TAKESHITA, MASAMICHI KOYANAGI, MAKOTO PI
                                                                                                                                                                                                                                                                                                                                                                                                         1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC
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                         /organism='Homo sapiens (human)'
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                                                                                                                                                                                                                                          100.0%; Score 228; DB 6;
Similarity 100.0%; Pred. No. 7.2e-57;
28; Conservative 0; Mismatches 0;
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Key Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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WO 0230464-A/2.
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SOURCE
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AUTHORS
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 228)

S Egashira,K., Yonemitsu,Y., Sueishi,K., Ikeda,Y. and Inada,Y.

Preventive or remedy for pulmonary hypertension

Datent: JP 2002047203-A 1 12.PEB-2002;

CS Homo sapiens (human)

PN JP-PRE-2002

PN JP-PN JP-PN
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00, A61P911/00, CO7K14/52, CO7K16/24//C12N15/09, A61K37/02, C12N15/00
Preventive or remedy for pulmonary hypertension FH Key
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                                                                                                WO 0189582-A/1
29-NOV-2001
25-MAY-2001 W 2001JP004381
25-MAY-2000 JP 00P 161145
KENSUKE EGASHIRA, YOSHIKAZU YONEMITSU, KATSUO SUEISHI, YASUHIRO
                                                                                                                                                                                                                                                                                  A61K48/00,A61K39/395,A61K38/17,A61K31/711,A61P11/00,A61P9/12
Composition for treating or preventing primary pulmonary CC
hypertension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                      TAKEDA CHEMICAL INDUSTRIES LTD, KENSUKE EGASHIRA, YOSHIKAZU
YONEMITSU, KATSUO SUEISHI, YASUHIRO IKEDA, YOSHIYUKI INADA
OS Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='Homo sapiens (human)'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT
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Preventive or remedy for pulmonary hypertension.
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100.0%; Score 228; DB 6;
Best Local Similarity 100.0%; Pred. No. 7.2e-57;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                    KOSHIYUKI INADA
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BD137507
LOCUS
DEFINITION
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AUTHORS
TITLE
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PAT 17-JAN-2003

linear

1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60 Gaps .; 0 Length 300; 0; Indels vuely match
Best Local Similarity 100.0%; Pred. No. 7.3e-57;
Matches 228; Conservative 0; Mismatches ο.

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00 da	CAGCCAGATGCAATCAATGCCCCCAGTCACCTGTTATAACTTCACCAATAGGAAGATC 129	BT007880	
Qy 61 7	TCAGTGCAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGAAGT 120	DEFINITION	Synthetic construct Homo sap
Db 130 7	TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 189	ACCESSION	380 380 380.1 GI
121	GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180	KEYWORDS SOURCE	Sonstruct
190	FIGAȚCTICAAGACCATIGIGGCCAAGGAGATCIGIGCIGACCCCCAAGCAGAAGIGGGTI 249	ORGANISM	synthetic construct artificial sequences.
Qy 181 C	CAGGATTCCATGGACACTGGACAAGCAAACCCAAACTCGAGACT 228 	AUTHORS	I (Lasses I CO 500) Kalnine, N., Chen, X., Rolfs, A Koundinya, M., Raphael, J., Mo Phelan. M. and Farmer, A.
6 6 6 6 6		TITLE	Cloning of human full-length
BD177097 LOCUS DEFINITION Pro	300 bp DNA linear PAT 16-APR-2003 pphylactic and/or remedy for vascular restenosis.	JOURNAL REFERENCE AUTHORS	Unpublished 2 (bases 1 to 300) Kalnine, N., Chen, X., Rolfs, P.
ACCESSION BD: VERSION BD: KEYWORDS JP SOURCE HOO	BD177097 BD177097.1 GI:30014357 JP 2002284698-A/2. Homo sepiens (human)	TITLE	Acundinya,M., Kaphaei,U., Mu Phelan,M. and Farmer,A. Direct Submission Submitted (13-MAY-2003) BD B
ORGANISM HOR	no sapiens karyota, Menazoa, Chordata, Craniata, Vertebrata, Buteleostomi,	COMMENT	Circle, Palo Alto, CA 94303, This CDS clone is a part of expression clones generated
REFERENCE 1 AUTHORS EGA	Illiania butterial filmares; cacailling, nominacy, nome. Bases 1 to 300) Bashira, K. and Takeshita, A.		Harvard Institute of Proteom forms: with and without stop
TITLE Pro	ophylactic and/or remedy for vascular restenosis lent: UP 202284699-A 2 3-00T-2005. Nemat: Antitut physokatemetra. On two		tag). The CDS has been dire cloning system between the S vector. Additional sequences
COMMENT OS			and before 'ATG' to provide last codon and before HindII
다. 11년 11년	03-OCT-2002 23-MAR-2001 UP 2001085073 KFNGTIKE FGASHTRA AKTRA TAKESHTTA	FEATURES source	Clone di
1 D Q	1K45/00, A61K31/711, A61K35/76, A61K38/00, A61K39/395, A61K39/395, PC		/organism="syntheti /mol_type="mRNA"
4 d d	A61K48/00, PC A61P9/10,A61P9/10/C12N15/09,A61K37/02,C12N15/00 CC		/db_xret="taxon:326 /clone="GH00237L1.0" /clone_lib="BD_Creations"
FI			collection" /lab_host="DH5alpha
BS	/organism='Homo sapiens (numan)'. Location/Qualifiers	CDS	10.000 \\ 1>300 \\ 1>300 \\ \ 1000 \\ 10
sonice	/ organism="Homo sapiens" /mol type="genomic DNA"		/codon_start=1 /trans1_table=11
ORIGIN	/db_xref="taxon:9606"		/product="Homo sap: /protein_id="AAP36! /db_xref="GI:30584!
Query Match	100.0%; Score 228; DB 6; Length 300;		/translation="MKVS/ VQRLASYRRITSSKCPKE
Matches 228	ive 0; Mismatcl	ORIGIN	
Qy 1 Db 70	CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60 	Query Match Best Local S Matches 228	tch al Similarity 100.0%; Pred 228; Conservative 0; Mi
Oy 61	TCAGTGCAGAGGTTCGCGAGGTATAGAAGAATCACCAGCAAGCA	ò	1 CAGCCAGATGCAATCAATGCCCCAG
Db 130	TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAAGTGTCTCCCAAAGAAGT 189	qa	70 CAGCCAGATGCAATCAATGCCCCAG
Qy 121		δλ	61 TCAGTGCAGAGGCTCGCGAGCTATA
Db 190	GTGATCTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 249	ga	
Qy 181	CAGGATTCCATGGACCACCTGGACAAGCCAAACTCCGAAGACT 228 CAGGATTCCATGGACACCTGGACAAGCAAACCAAACCA	δ Q	121 GTGATCTTCAAGACCATTGTGGCCA.
		λŎ	181 CAGGATTCCATGGACCACCTGGACA

RESULT 5

Jus, use a collection of human full length ted by B biosciences Clontech and the tedmics. Bach CDS has been cloned in two stepp-coden (to allow fusion with C-terminal directionally cloned using BD In-Fusion (TM) he sall and hindil sites of the pDNR-DDAL mide in the clone: 'ACC' after Sall site ride Kozak consensus sequence; 'GG' after andIII site to maintain reading frame.

Alli site to maintain reading frame. SAALLCLLLIAATFI PQGLAQPDAINAPVTCCYNFTNRKIS EAVI FKTI VAKEI CADPKQKWVQDSMDHLDKQTQTPKTL" ö A., Halleck, A., Hines, L., Eisenstein, S., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., A., Halleck, A., Hines, L., Eisenstein, S., foreira, D., Kelley, T., LaBaer, J., Lin, Y., GTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60 AGAAGAATCACCAGCAAGTGTCCCAAAGAAGT 120 AAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180 00 bp mRNA linear SYN 13-MAY-2003 apiens chemokine (C-C motif) ligand 2 Biosciences Clontech, 1020 East Meadow 3, USA eator(TM) CDS Library derived from MGC h CDSs in BD Creator (TM) System Donor piens chemokine (C-C motif) ligand 2" 6552.1" 4599" 0; Gaps cd. No. 7.3e-57; Length 300; cd. No. 7.3e-57; lismatches 0; Indels 0; CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228 ha T1 resistant" NR-Dual" 299:Stop->Leu" cic construct" 2630" 181 δ

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Yamagishi, J., Mateuo, T., Fukui, J. and Yamada, M.
PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYPEPTIDE AND MICROBIAL STRAIN PRODUCING THE POLYPEPTIDE

AL PACHT: JP 1993C60987-A 3 12-OCT-1993;

DAINIPPON PHARMACEUT CO LTD

PN JP 1993E60987-A/3

PF 12-OCT-1993;

PR 02-MAY-1991 JP 91P 135950

PI YAMAGISHI JUNICHI, MATSUO TOKUYUKI, FUKUI JUICHI, PI YAMADA MASAAKI

PC 012P21/02,C12N1/21//C12N15/12,(C12P21/02,C12R1:19),(C12N1/21, CC strandedness: Double;

CC strandedness: Double;

CC anti-sense: No;

CC anti-sense: No;

CC anti-sense: No;

FT Key

FT RES

FT S'UTR

11.39

FT RES

FT AOTOR

AO: 2577

FT AOTOR

CDS

AO: 2770

FT AOTOR

FT AOTOR

CDS

FT AOTOR

AO: 2770

FT AOTOR

FT AOTOR

AO: 2770

AO
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100.0%; Score 228; DB 6;
Best Local Similarity 100.0%; Pred. No. 7.4e-57;
Matches 228; Conservative 0; Mismatches 0;
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/organism="synthetic construct"
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Sequence 72 from Patent W002063030.
AX698741
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1. 554
Acgains="Escherichia oc/mol_type="genomic RNA"
/db_Xref="taxon:562"
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          AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                          artificial sequences.
The bases 1 to 418)
Yamagishi, J., Matsuo, T., Fukui, J. and Yamada, M.
PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYPEPTIDE AND MICROBIAL STRAIN PRODUCING THE POLYPEPTIDE
PATENTA PRODUCING THE POLYPEPTIDE
PATENT: JP 1993256087-4 19 12-OCT-1993;
DAINIPPON PHARMACEUT CO LTD
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Enterobacteriaceee; Escherichia.
1 (bases 1 to 554)
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09-WAY-1991 JP 91P 135950
YAWAGISHI JUNICHI, MATSUO TOKUYUKI, FUKUI JUICHI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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       250 CAGGATICCAIGGACCACCIGGACAAGCAAACCCAAACICCGAAGACI 297
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100.0%; Pred. No. 7.4e-57;
ive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                               DNA
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Artificial sequence, Genes.
JP 1993260987-A/19
12-OCT-1993
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strandedness: Single;
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hypothetical: No;
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JP 1993260987-A/3.
Escherichia coli
Escherichia coli
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synthetic construct
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Matches 228; Conservative
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E05615.1 GI:21
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E05599
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ô Lyamichev, V., Skrzpczynski, Z., Allawi, H.T., Wayland, S.R., Takova, T. and Neri, B.P.
Charge tags and separation of nucleic acid molecules
Patent: WO 02063030-A 72 15-AUG-2002;
THIRD WAVE TECHNOLOGIES, INC. (US) PAT 02-APR-2003 120 100 TCAGTGCAGAGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 159 180 160 GTGATCTTCAAGACCATTGTGGCCCAAGGAGTTCTGTGCTGACCCCAAGCAGAAGTGGGTT 219 9 99 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 40 cacccacariccariccariccccacricacricritaraacricaccaaraccaaca TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT Gaps . 267 181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228 Length 554; CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT Indels linear

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Gaps

182 120

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PAT 09-JUL-2003
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                             Cocks, B.G. Stuart, S.G. and Seilhamer, J.J.
Cocks, B.G. Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and
response gene expression
Patent: US 6607879-A 1344 19-AUG-2003;
Location/Qualifiers
1. 775
/organism="unknown"
/mol_type="genomic DNA"
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Methods for assessing and treating leukemia
Patent: WO 03038129-A 58 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
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Pred. No. 7.5e-57;
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    .725
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Sequence 58 from Patent WO03038129.
AX774742
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                                  Unclassified.
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                Unknown
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les 228;
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                                                                                                                                      1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                       Gaps
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Unknown.
Unknown.
Unclassified.
I (bases 1 to 725)
Garzino-beno,A. and DeVico,A.L.
Immuno-modulating effects of chemokines in DNA vaccination
Patent: US 6569418-A 3 27-MAY-2003;
Location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 3 from patent US 6569418.
AR337874
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AR380799
AR380799.1 GI:40088433
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182 120 242 180 302

PAT 08-JAN-2003

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123 cagccagargcaarcaargcccagrcaccrgcrgrraraacrrcaacaaraggaagarc 182
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                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Yoshimura, T. and Leonard, E.J.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                Garcia,T., roman Roman,S., Baron,R., Call,K., Theilhaber,J., Connolly,T., Jackson,A., Bushnell,S.E. and Rawadi,G. Genes involved in osteogenesis, and methods of use Patent: WO 02081745-A 96 17-OCT-2002; Aventis Pharma S.A. (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s/1513 739 bp mRNA linear PRI (monocyte chemoattractant protein-1 [human, mRNA, 739 nt].
871513
303 CAGGATICCAIGGACCACCIGGACAAGCAAACCCAAACTCCGAAGACT 350
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Adv. Exp. Med. Biol. 305, 47-56 (1991)
92095166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 100.0%; Score 228; DB 6; al Similarity 100.0%; Pred. No. 7.5e-57; 228; Conservative 0; Mismatches 0;
                                                                                                                             DNA
                                                                                                                       739 bp | Sequence 96 from Patent WO02081745. AX577974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Codon start=1

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/procedin id="CAA32876.1"

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                                                                                                                                                    HSMCP1 725 bp mRNA linear PRI 03-APR-1995
H.sapiens mRNA for monocyte chemoattractant protein 1 (MCP-1).
X14768
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitogen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JE FBES Lett. 244 (2), 487-493 (1989)
245524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
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                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 725)
Yoshimura,T., Yuhki,N., Moore,S.K., Appella,E., Lerman,M.I. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGCCAGATGCCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                      181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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/note="pot. N-linked glycosylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 228; DB 9;
ilarity 100.0%; Pred. No. 7.5e-57;
Conservative 0; Mismatches 0;
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/product="MCP-1 (AA 1 - 76)"
162, .170
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/clone_lib="lambda" cells"
54. .353
                                                                                                                                                                                                                                                     monocyte chemoattractant protein 1.
Homo sapiens (human)
Homo sapiens
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/note="polyA site"
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121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180
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139 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGAAAGATC 198
                                                                                                                199 TCAGTGCAGAGGTCGCGAGCTATAGAAGAATCACCAGCAGCAGTGTCCCAAAGAAGCT
                                                                         61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
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Search completed: August 31, 2004, 03:22:47 Job time : 1394 secs

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54. 353
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                                                      'gene="monocyte chemoattractant protein-1, MCP-1"
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/db_xref="taxon:9606"
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741 bp

A17786.1 GI:641144

A17786 MCP-1 mRNA. A17786

RESULT 15
A17786
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
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SOURCE
ORGANISM

unidentified
unidentified
unidassified.
1 (bases 1 to 741)
Caput, D., Ferrara, P., Miloux, B., Minty, A. and Vita, N.
Protein with cytokine activity, recombinant DNA, expression vector and hosts for obtaining it
Patent: EP 0488900-A 25 03-JUN-1992;
ELF SANOFI

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

; 0

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1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGTTATAACTTCACCAATAGGAAGATC 60

Query Match 100.0%; Score 228; DB 6; Length 741; Best Local Similarity 100.0%; Pred. No. 7.5e-57; Matches 228; Conservative 0; Mismatches 0; Indels (

ORIGIN

(oideu) Anola agod sini

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 30, 2004, 16:49:10 ; Search time 236 Seconds (without alignments) 4104.191 Million cell updates/sec Run on:

Title: Perfect score:

3373863 seqs, 2124099041 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_29Jan04:*

1: geneseq11980s:*

2: geneseq11980s:*

4: geneseq12001as:*

5: geneseq1201as:*

6: geneseq1201s:*

7: geneseq12013s:*

8: geneseq12013s:*

9: geneseq12013s:*

9: geneseq12013s:*

10: geneseq12013s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOUTH THE SOUTH	Length DB ID De	.00.0 228 6 ABA02497 Aba02497 Human mon	.00.0 300 6 ABL60575 Abl60575 Human mon	00.00	0 475 6 ABV97697 Abv97697	647) 725 2 AAQ85370 Aaq85370	.00.0 725 2 AAX80631 Aax80631 Monocyte		00.0 725 9 ADD18494 Add18494	00.0 725 9 ADE84839 Ade84839		0 739	739 6 ABV78071 Abv78071	7 ABZ34738 Abz34738	741 3 AAA34899	741	0 741	0	0 802 2 AAZ33515	0 804	978	
dk	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		000
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Aav34249 Human sec	Acd08120 cDNA enco	Aav34248 Human sec					Aav86197 EST clone	Aag30749 MCF (DraI		Aag30745 MCF (SS)		Aag30748 pHMCF7. 3	_	Aag30746 MCF (DS)	Aaa44418 Human sec	Aav86195 EST clone	Abl60574 Human mon	Acc42733 Monocyte	Aba02498 Human mut	Aax24805 Human mon	Aav88315 EST clone
AAV34249	ACD08120	AAV34248	ACD08119 .	AAQ05625	AAT03528	AAV86200	AAV86197	AAQ30749	ABV96715	AAQ30745	AAA74882	AAQ30748	AAT48092	AAQ30746	AAA4418	AAV86195	ABL60574	ACC42733	ABA02498	AAX24805	AAV88315
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227.6	227.6	227.6	227.6	227.2	226.4	226.4	226.4	226.4	226.4	226.4	226.4	226.4	224.8	221.6	220.4	211.2	205.2	205.2	204	196	193.2
24	25	56	27	28		30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human, monocyte chemoattractant protein-1, MCP-1, C-C chemokine family, pulmonary hypertension, primary, hypotensive, gene, ds. replace(3..25, GG) /*tag= b /nce= "The sequence encoding the 7ND-MCP-1 mutant /NDR6== "The sequence a 24 bp deletion relative to this sequence" /*tag= a /partial /product= "Human MCP-1" /note= "No start or stop codon given in the specification" Human monocyte chemoattractant protein-1 (MCP-1) DNA. Location/Qualifiers ABA02497 standard; DNA; 228 BP. 25-MAY-2001; 2001WO-JP004381. 26-MAR-2002 (first entry) 1. .228 /*tag= < WO200189582-A1. Homo sapiens. 29-NOV-2001. ABA02497; mutation RESULT 1 ABA02497 HANDER STANDER STANDER

26-MAY-2000; 2000JP-00161145.

(TAKE) TAKEDA CHEM IND LTD. (EGAS/) EGASHIRA K.

WPI; 2002-083059/11. P-PSDB; AAM53048.

Egashira K, Yonemitsu Y, Sueishi K, Ikeda Y, Inada Y;

Preventives and remedies for pulmonary hypertension containing mutant of MCP-1 antagonistic inhibitory type or its salt, encoded DNA or

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Sequence 300 BP; 83 A; 88 C; 68 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 228;
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                                                                                                  Matches 228; Conservative
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                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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Best Local
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                                          The invention relates to preventives and remedies for pulmonary hypertension, comprising an antegonistic inhibitory mutant of monocyte chemoattractant protein-1 (MCP-1), DNA encoding the mutant MCP-1, or a neutralising antibody against MCP-1. MCP-1 is a member of the C-C chemokine family. The preventives and remedies have hypotensive activity and can be used in the prevention and treatment of pulmonary hypertension particularly pulmonary primary hypertension. The present sequence represents DNA encoding wild-type human MCP-1.
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                                                                                                                                                                                                                                                                                                                     GTGATCTTCAAGACCATTGTGGCCAAGAGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                  CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                      CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                   CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAAACTCCGAAGACT
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                                                                                                                                               Sequence 228 BP; 71 A; 62 C; 53 G; 42 T; 0 U; 0 Other;
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                                                                                                                                                                     100.0%; Score 228; DB 6;
100.0%; Pred. No. 3.4e-62;
tive 0; Mismatches 0;
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                      Page 32; 39pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL60575 standard; DNA; 300 BP
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 neutralization antibody
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EGASHIRA K.
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                                                                                                                                                                               Local Similarity
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                     Disclosure;
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function inhibitor as the active ingredient. The MCP-1 function inhibitors are useful in treating and preventing hepatic diseases such as liver fibrosis or liver cirrhosis. The present sequence represents a human MCP-1 related DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
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                                                                                                                                                                                                                          Length 300;
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                                                                                                                                                          Sequence 300 BP; 83 A; 88 C; 68 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                       Score 228; DB 6;
Pred. No. 3.8e-62;
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DB 7; Length 300;

ö The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP66596-ABP66637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer 129 120 190 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT 249 130 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 189 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180 9 New isolated polynucleotide and pancreatic tumor polypeptides, useful f diagnosing, preventing and/or treating cancer, particularly pancreatic CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 70 cadecadardeaardaccecadreacerdergranaacrreaceaaragaare TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGAAGTGTCCCAAAGAAGCT Gaps Jiang Y; therapy; vaccine; immunostimulant; · 0 228 Claim 1; SEQ ID NO 3105; 300pp + Sequence Listing; English. CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT Hepler WT, Indels Human pancreatic cancer expressed cDNA SEQ ID NO 3105. Pred. No. 3.8e-62; Mismatches 0; Persing DH, 100.08; Lodes MJ, BP. Conservative Similarity 228; -61 121 181 Best Local Matches 22 Db à g ò g à

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and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                          345
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                                                                                                                                                                                                                                                                                                                                                                                                                                284 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCTGACCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                   404 CAGCCAGATCCAATCAATGCCCCAGTCACCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                   61 TCAGTGCAGAGGTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
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                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 177
                                                                                                                                                                                  Length 475;
                                                                                                                                                 Sequence 475 BP; 134 A; 90 C; 122 G; 129 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lyamichev V, Skrzpczynski Z, Allawi HT, Wayland SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human monocyte chemoattractant protein-1 (hMCP-1) RNA
                                                                                                                                                                                    100.0%; Score 228; DB 6; 1
100.0%; Pred. No. 4.6e-62;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (THIR-) THIRD WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-FEB-2002; 2002WO-US003423
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Best Local Similarity 100.
Matches 228; Conservative
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Query Match

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Location/Qualifiers
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                                                                                                                   Similarity
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molecules, the method provides an absolute readout of the partition of products from substrates (i.e. provides a 100% separation). Through the use of multiple positively charged adducts, synthetic molecules can be constructed with sufficient modification due to the fact that the normally negatively charged strand is made nearly neutral. It is also possible to distinguish between a enzymatically or thermally degraded DNA fragments due to the absence or presence of 3'phosphate. ABS60740-ABS60813 represent coding sequences and primers used in the method of the
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                                                                                                                                                                                                                                                                                                        CAGUGCAGAGGCUCGCGAGCUAUAGAAGAAUCACCAGCAGCAAGUGUCCCCAAAGAAGGAGCU 189
                                                                                                                                                                                                                                                TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                              GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180
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                                                                                                                                                                                                                                                                                                                                                                GUGAUCUUCAAGACCAUUGUGGCCAAGGAGAUCUGUGCCCGAAGCCAAGGAGGGGUU
                                                                                                                                                                                                      Gaps
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                                                                                                                                             Sequence 647 BP; 180 A; 146 C; 121 G; 0 T; 200 U; 0 Other;
                                                                                                                                                                                                     Indels
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                                                                                                                                                                       %; Score 228; DB 6;
; Pred. No. 5.2e-62;
42; Mismatches 0
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93US-00136117.
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nes 186; Conservative 4
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29-AUG-1995
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AAQ85370 ID AAQ

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reverse transcription of mRNA from activated human leukocytes, then clouing of the cDNA into pVL1392 bacultovirus vector, and expression in Sf9 cells in the presence of reduced glutathione and dithiothreitol. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 Grearcricaadaccarneredeccaageaarcrerereacccaagcagaagregerr
                                                                                                                                                                                                                                                                                                                                                                       CAGCCAGATGCAATGAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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product= "Monocyte chemoattractant preprotein"
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                                                                                                                                                                                                                                      Length 725;
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label= Monocyte_chemoattractant_protein_l
_______nchemotactic for monocytes"
                                                                                                                                                                       Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                   100.0%; Score 228; DB 2;
100.0%; Pred. No. 5.4e-62;
ive 0; Mismatches 0;
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(MCP-1) DNA
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                                                             The present sequence encodes monocyte chemoattractant protein-1. The efficacy of a vaccine is enhanced by combining it with one or more chemokines. This can be used to enhance humoral or cell-inediated immune response. The purified nucleotide sequence encoding the chemokine, fragments, derivatives, analogues, or truncation isoforms are expressed in a coordinated manner upon introduction in a suitable cell. These sequence are operably linked to one or more gene regulatory elements. The nucleic acid may have deletional, insertional, or substitutional mutations. They are referred as DNA vaccines and are administered by constructing an expression plasmid vector either directly or indirectly. The chemokine gene is isolated by PCR, which can be used to amplify the desired sequence in a genomic or cDNA library. The vaccines can be used to treat microbial diseases especially HIV
                                                                                                                                                                                                                                                                                                      123 CAGCCAGATGCAATGAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 182
                                                                                                                                                                                                                                                                                                                                    TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                          immune response; vaccine; macrophage derived chemokine; MDC; IV; virucide; immunostimulant; monocyte chemoattractant protein 1;
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                                                                                                                                                                                                                                           100.0%; Score 22%; DB 2; Length 725; 100.0%; Pred. No. 5.4e-62; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                         Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human monocyte chemoattractant protein 1 (MCP-1) DNA.
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                      of enhancing vaccine efficacy
                                             Claim 22; Page 65-66; 134pp; English
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02-MAR-2000; 2000US-0186416P.
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                                                                                                                                                                                                                                                                      228; Conservative
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  P-PSDB; AAY26176.
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prostate tissue; cancer diagnostic; cancer marker; prostate cancer; PCA; male cancer-related death; serum biomarker; tissue biomarker; cytostatic; gene therapy; prostate biopsy tissue; AMACR; alpha-methylacyl-coenzyme A racemase; diagnosing cancer; cell growth; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                           The invention relates to a method for improving immune response to an HIV antigen. The method involves administering to the subject a composition which comprises: an isolated HIV antigen (e.g., apl20 or gp160) against which an immune response is desired in subject, chemokine, such as macrophage derived chemokine (MDC) and a carrier. The method is useful for improving subject's immune response to HIV antigen (e.g., gp120 or gp160). The invention is useful for enhancing the efficacy of immune response against the antigen in a subject. The invention is useful as
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administering composition gp160, a macrophage derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e-62;
Matches 228; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
     Improving immune response to HIV antigen by which comprises an antigen such as gp120 or chemokine, and carrier.
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                                                                                                                  Disclosure, Col 19-20; 40pp; English.
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15-NOV-2001; 2001US-0334468P.
01-AUG-2002; 2002US-00210120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD18494 standard; DNA; 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003012067-A2
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This invention relates to a novel method of characterising prostate tissue in a subject and to compositions and methods for cancer diagnostics, including cancer markers, in particular prostate cancer. Prostate cancer (PCA) is a leading cause of male cancer-related death. Additional serum and tissue blomarkers would aid diagnosis. The invention may provide means of producing compounds with a cytostatic activity or allow the development of gene therapy. The methods of the invention useful for characterising prostate tissue in a subject, screening subject, detecting AMACR (alpha-methylacyl-coenzyme A racemaes) expression in a bodily fluud, characterising the growth of cells. The diagnosing cancer in a subject and inhibiting the growth of cells. The present sequence is a DNA sequence which is preferably utilised in the
                                                           Characterizing prostate tissue comprises providing a prostate tissue sample from a subject and detecting the presence or absence of expression of hepsin, pim-1 or EZH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 cagccagardcaarcaargccccagrcacrdcrdrraraacrrcaccaaraggaagarc 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIGATCITCAAGACCATTGIGGCCAAGGAGATCTGIGGCTGACCCCCAAGCAGAGTGGGT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Farnesyl transferase inhibitor modulated leukemia associated gene #58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ss; cytostatic; farnesyl transferase inhibitor; gene expression;
quinolinone; leukemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGATTCCATGGACCTGGACAAGCAAACCCAAACTCCGAAGACT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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100.0%; Pred. No. 5.4e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                 Disclosure; SEQ ID NO 66; 297pp; English.
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2001US-0340938P.
2001US-0341012P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     method of the invention.
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30-OCT-2001;
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ID ADB84
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The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B) 6-[amino(4-chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl) -1-methyl-2-(IA)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human monocyte chemo-attractant peptide; inflammatory disease; neoplasms;
                                                                              Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAGCCAGATGCAATCCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 TCAGTGCAGAGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAGTGTGCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA which encodes human monocyte chemo-attractant peptide-1.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 228; DB 9; Best Local Similarity 100.0%; Pred. No. 5.4e-62; Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                 Disclosure; SEQ ID NO 58; 346pp; English
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/*tag= c
/label= mature MCP-1
705. 709

/*tag= b
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53. .350
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(revised)
(first entry)
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                                                WPI; 2003-513497/48.
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17-DEC-2001
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                 Raponi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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AAN91337
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USN7330446-N.

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The present sequence encodes a monocyte chemoattractant peptide (MCP) designated MCP-1. MCPs can be isolated from human glioma cell line U-105MG and peripheral blood monomuclear leukocytes. MCPs are used for the treatment of neoplasms and infections in humans. Short peptides derived from MCPs can be screened to identify those that can bind to the monocyte receptor without stimulating a chemotactic response. These are potentially useful for treating inflammation associated with monocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 chdarchrcaagaccarhdregeccaaggachtergrerereaccccaagcagaagreedri 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide with chemotactic activity for monocytes - from human monocytes or glioma cells, useful for treating infections and neoplasms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rcagigcagaggcrcagaggranagaagaarcaggaggaagrgcccaaagaaggrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 739 BP; 222 A; 174 C; 123 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT
               /*tag= a
/transl_except= (pos: 54. .56, aa: Met)
/transl_except= (pos: 114. .116, aa: Gly)
707. .711
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.4e-62;
                                                                                                                                                                                                                                                                                                                                                                             Robinson EA, Yoshimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypoxia-regulated protein coding sequence #91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                     DEPT HEALTH & HUMAN SERVICES
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89US-00330446
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                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-129909/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW40174
                                                                                                                                                                                                                                                                        31-JAN-1989;
30-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infiltration
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                                                                                                                                                                                                                               06-JUN-1995;
                                                                                 polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                  Leonard EJ,
                                                                                                                                              US5714578-A
                                                                                                                                                                                    03-FEB-1998
                                                                                                                                                                                                                                                                                                                                     SO (HSSO)
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                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence encodes a human-derived monoyte chemo-attractant peptide product (MCP-1) which exhibits optimal chemotactic activity at a conco. of 1nM and has a mol. mass of ca. 8,400 D. MCP-1 can be used for treating infection eg inflammatory disease, or for the control of neoplasms by accumulation of monocytes at the site of the infection. The DNA is obtd. by chemical synthesis, by screening reverse trascripts of mRNA from purified blood leukocytes or cell cultures of eg U-373 MG or KMG-5. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with orgaing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpl/updates/ntis_us.html.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                       obtd. from human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCCAGATGCAATGAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                   Human derived monocyte chemo:attractant peptide prods. - obtd. from h
glioma cell line U-105MG or peripheral blood mono:nuclear leukocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding a macrophage chemoattractant peptide designated MCP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGATTCCATGGACCACCTGGACAAGCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 228; DB 1; Length 738; 100.0%; Pred. No. 5.4e-62; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 738 BP; 221 A; 170 C; 127 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                               되.
                                                                                                                                                                                                               Leonard
                                                                                                                     DEPT HEALTH & HUMAN SERVICE.
SEC OF COMMERCE.
SEC OF COMMERCE.
                                                                                                                                                                                                               Appella E,
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                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 2; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВР
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                                             89US-00330446
                                                                                   89US-00304234
                                                                                                                                                                                                                  Yoshimura T, Robinson EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228; Conservative
                                                                                                                                                                                                                                                          WPI; 1989-300683/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                            P-PSDB; AAP95387
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                                             30-MAR-1989;
                                                                                     31-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1998
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    25-JUL-1989
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Query Match

Best Loca Matches

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121

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Indels

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120 242 180

182

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The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABN77873-ABN78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conditions, and for regulating tumourigenesis, angiogenesis, apoptobles, balological response to hypoxia conditions, or hypoxic-associated balological response to hypoxia conditions, or hypoxic-associated for monitoring the therapeutic treatment of a disease or physiological for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, precelapmsia atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ischaemic condition, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory condition, wound healing, inflammation; erythropoiesis, hair loss, human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two celltypes under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 digarcricaagaccarreregecaagaagarcrereregececaagcagaagreegri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 228; DB 6; Length 739;
Pred. No. 5.4e-62;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 739 BP; 222 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT
                                                                                                                                                                                                                                                                                                                                                                                        Ward NR, Krige D, Kingsman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 37; Page 399; 538pp; English.
                                                                                                                                                                                                                                                                                                                                             (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                              08-FEB-2001; 2001GB-00003156.
25-OCT-2001; 2001GB-00025666.
                                                                                                                                                                                                                 10-DEC-2001; 2001WO-GB005458
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Conservative 0
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                                                                                                                              WO200246465-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulated gene
                                                                                                                                                                                                                                                        08-DEC-2000;
                                                                                     Homo sapiens
                                                                                                                                                                      13-JUN-2002
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Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                        Rayner WN;
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two cell

Harris RA;

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differentially expressed in models of osteogenesis upon being put in contact with a stimulator of osteogenesis. The present sequence is one such sequence. This sequence can be used for diagnosing osteoporosis/bone disease in a patient, promoting osteogenesis and/or preventing osteoporosis/bone disease. The present sequence encodes a secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGATCTTCAAGACCATTGTGGCCAAGGAGTCTGTGCTGACCCCAAGCAGAAGTGGGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention relates to novel nucleotide sequences, which are
                                                                                                                                                                                                                                                                                                                                                                                                         isolated nucleic acid upregulated/downregulated in osteogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 CAGCCAGATGCAATCAATGCCCCAGTCACCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                               Osteopathic; osteogenesis modulator; gene therapy; osteogenesis; osteoporosis; bone disease; downregulator; human; ss.
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                                                                                                                                                                                                                                                                                                                                 Theilhaber J;
G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT
                                                                                  Coding sequence SEQ ID 96, downregulated in osteogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 228; DB 7;
100.0%; Pred. No. 5.4e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                 Call K, '
                                                                                                                                                                                                                                                                                                                                                                                                                       for bone disease therapy in subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Page 124-125; 237pp; English.
                                                                                                                                                                                                                                                                                                                                   Baron R, C
BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВЪ
                                                                                                                                                                                                                                             05-APR-2002; 2002WO-IB002211.
ABZ34738 standard; cDNA; 739
                                                                                                                                                                                                                                                                          05-APR-2001; 2001US-0281400P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA34899 standard; DNA; 741
                                                                                                                                                                                                                                                                                                    (AVET ) AVENTIS PHARMA SA.
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Best Local Similarity 100.
Matches 228; Conservative
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                                                                                                                                                                                      WO200281745-A2
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Connolly T,
                                                       04-FEB-2003
                                                                                                                                                                                                                 17-OCT-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                         Novel
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182 120 242 180

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Gaps

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9

120 242 180 302

RESULT 14 ABZ34738

Human adenosine receptor related polynucleotide SEQ ID NO:2588.

phosphorothioate; impaired respiration; infilammation; allergy; allergy; allergy; antialground-construction; inhibitor; antiantiantantant antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss. adenosine receptor; low adenosine antisense oligonucleotide; WO200009525-A2 Homo sapiens.

24-FEB-2000.

99WO-US017712. 03-AUG-1999;

98US-0095212P. 03-AUG-1998;

(UYEC-) UNIV EAST CAROLINA

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or

Disclosure; Page 761-762; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (CN) with low adenosine (up to 15%), which targets conclete acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, confined airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating c. impeded respirations, pulmonary vasconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive fibrosis, and cancers which map metastasis to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the carcinomas, and cancers which may metastasis to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the calease of deoxyadenosine which activates adenosine receptors causing conchoconstriction and inflammation. AAA12313 to AAA3531 represent to invention, which correspond to SEQ ID No:1 to 2815, and then the last 185 sequences are also called SEQ ID No:1 to 2815, and then the last to the previously named sequences. SEQ ID No:1 to 1680 (AAA3233 to AAA3392) are specifically claimed ONS from the present invention. N B. Sequences given in the disclosure of the present invention of ont match is the interpretation of the present invention. On the interpretation of the present invention. On the interpretation of the present invention. isting

Sequence 741 BP; 214 A; 173 C; 133 G; 221 T; 0 U; 0 Other;

ö 9 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 0; Gaps 100.0%; Score 228; DB 3; Length 741; 100.0%; Pred. No. 5.5e-62; ive 0; Mismatches 0; Indels C Query Match 100. Best Local Similarity 100. Matches 228; Conservative 8

139 cadecadardecardecardececeardecerderaraacerrecearadeaagare 198

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258 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 199 readrecadadecredecadecraradadaareaceaceageaagrereceaaaager 61

121 GIGAICTICAAGACCATIGIGGCCAAGGAGAICTGIGCTGACCCCAAGCAGAAGIGGGIT 180 259 grgarctrcaagaccarreregeccaaggagcrcrcrerecreaccccaagcagaagregerr 318 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228 319 caggarrccarggaccaccrggacaagcaaacccaaacrccgaagacr 366 181 g 8 엄 à

completed: August 31, 2004, 02:58:29 he: 241 secs Search cor Job time

Luis Page Blank (uspio)

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on:

August 30, 2004, 16:49:11; Search time 54 Seconds (without alignments) 2343.126 Million cell updates/sec

07330446 228 1 cagccagatgcaatcaatgc.....aaacccaaactccgaagact 228 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 seqs, 277475446 residues Searched:

1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/pcTuS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 13.4 Appli Sequence 15.5 Appli Sequence 10.5 Appli Sequence 10.5 Appli Sequence 10.5 Appli Sequence 2.7 Appli Sequence 2.7 Appli Sequence 2.7 Appli Sequence 17.3 Appli Sequence 17.3 Appli Sequence 17.4 Appl Sequence 17.5 Appli Sequence 17.5 Appli Sequence 26.7 Appli Sequence 27.7 Appli	
QI	US-09-591-992-3 US-09-521-31-25 US-09-148-55-1165 US-09-148-545-106 US-09-148-545-106 US-09-148-545-105 US-09-148-545-105 US-09-148-545-105 US-09-148-545-105 US-09-148-123 US-09-148-123 US-09-148-123 US-09-148-123 US-09-16-31-13 US-09-16-31-15 US-09-023-655-901 US-09-023-655-978 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-016-434-1156 US-09-463-458A-8	
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Score	222222 11 2222222222222222222222222222	
Result No.	0 111111111111111111111111111111111111	

RESULT 2 US-09-023-655-1344 ; Sequence 1344, Application US/09023655

Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 687, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 39, Appli Sequence 39, Appli Sequence 38, Appli Sequence 38, Appli Sequence 38, Appli Sequence 45, Appli Sequence 45, Appli Sequence 45, Appli Sequence 45, Appli Sequence 45, Appli Sequence 45, Appli	1229, 21, A
US-08-613-822-3 US-08-852-212-1 US-09-479-729B-3 US-09-261-201A-3 US-09-717-209-3 US-09-016-44-687 US-09-545-894-1 US-09-546-0887A-5 US-09-646-028-44 US-09-646-028-37 US-09-646-028-37 US-09-646-028-37 US-09-646-028-37 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38 US-09-646-028-38	-09-833-381-12 -09-366-887A-2
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ALIGNMENTS

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APPLICANT: MILOUX, Brigitte
APPLICANT: MILOUX, Adrian
APPLICANT: MINTY, Adrian
APPLICANT: MINTY, Adrian
APPLICANT: MINTY, Adrian
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
CORFACING SYSTEM: PC-DCS/MS-DCS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/927,391
FILING DATE: 1992029
CLASSIFICATION: 530
ATTONNEY/AGENT INFORMATION:
NAME: SAXE: Bernhard
D REGISTRATION NUMBER: 28,665
REPRENCE/DOCKET NUMBER: 16781/369
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELBERGE (700.
TELERS: 899149
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
""R: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                       ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
FERRARA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                              VIRGINIA
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US-09-023-655-1165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242
                                        APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 228; DB 4; Length 725; 100.0%; Pred. No. 3.8e-61; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION NUMBER: US/09/023,655 FILING DATE: HEREWITH
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: PA-0001 US
TELECHONE: (650) 855-0555
TELECHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1344:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                 CITY: PALO ALTO STATE: CALIFORNIA
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                          GENERAL INFORMATION:
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US-09-023-655-1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: line IMMEDIATE SOURCE
  Patent No. 6607879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 228;
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Patent No. 6607879
GENERAL INFORMATION:
GENERAL SCACKS, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Cocks Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                             1 CAGCCAGATGCAATCCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                       199 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
                                                                                0; Gaps
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Query Match
100.0%; Score 228; DB 3; Length 741;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 228; Conservative 0; Mismatches 0; Indels (
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%Sequence 25, Application US/07927391; Sequence 25, Application US/07927391; Parent No. 601649; GENERAL INFORMATION: APPLICANT: CAPUT, Daniel

Wed Sep

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139 CAGCCAGATGCATATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATG 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 GIGAICTICAAGACCATIGIGGCCAAGGAGAICIGIGCIGACCCCAAGCAGAAGIGGGII 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60
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                                                                                                                                                COUNTRY: USA

ZIP: 94304

COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 37,071
PRIOR APPLICATION:
TALSSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 660) 845-4166
INFORMATION FOR SEC ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STOPOLGY: linear
INMEDIATE SOURCE:
LENGTH: G18734
US-09-023-655-1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-148-545-106
; Sequence 106, Application US/09146545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TILE OF INVENITON: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER FILING DATE: 1998-03-06
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
STREET: 3174 PORTER DRIVE
STREET: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 228; Conserva:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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ERRLIER PILLING DATE: 1997-03-07
ERRLIER APPLICATION NUMBER: 60/040,333
ERRLIER APPLICATION NUMBER: 60/040,626
ERRLIER APPLICATION NUMBER: 60/040,626
ERRLIER PILLING DATE: 1997-03-07
ERRLIER PILLING DATE: 1997-03-07
ERRLIER FILLING DATE: 1997-03-03
ERRLIER FILLING DATE: 1997-03-03
ERRLIER FILLING DATE: 1997-03-03
ERRLIER FILLING DATE: 1997-05-23
ERRLIER FILLING DATE: 1997-05-03-07
ERRLIER FILLING DATE: 1997-05-03-07
ERRLIER FILLING DATE: 1997-05-03-07
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R APPLICATION NUMBER: 60/056,864
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R FILING DATE: 1997-05-23
R PELLING DATE: 1997-05-23
R FILING DATE: 05-8ep-1997
R APPLICATION NUMBER: 60/047,599
R APPLICATION NUMBER: 60/047,588
R APPLICATION NUMBER: 60/047,588
R FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,313
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
                                                                                                                                                          LING DATE: 1997-06-06
PLICATION NUMBER: 60/056,886
LING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,872
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/056,882
FILING DATE: 1997-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/056,637
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,903
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APPLICATION UNDRER: 60/056,892
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/047,595
                                                                                                                                                                                                                                               FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
                                                                                                                                                                                                                                                                                                                                                                                                                               LING DATE: 1997-08-22
PLICATION NUMBER: 60/056,662
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FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/056,911
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,594
                                                                                                                                                                                                                            APPLICATION NUMBER: 60/056,877
                                                                                                                                                                                                                                                                                                                  PLICATION NUMBER: 60/056,893
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/056,630
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/056,878
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLICATION NUMBER: 60/056,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/056,894
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/056,874
                                                                                                                                                                                                                                                                                                                                    1997-08-22
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                                                                    1997-04-11
                                                                                                                                                                                                                                                                                            1997-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-08
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1119 TCAGTGCAGAGGTTCGCGAGCTATAGAAGAATCACCAGCAGCAAGGAGTGTCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.8%; Score 227.6; DB 4; Length Best Local Similarity 99.6%; Pred. No. 6.9e-61; Matches 227; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 105, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-12
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-08-22
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US-09-148-545-105
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CURRENT PELLING DATE: 1998-09-04

EARLIER PELLING DATE: 1998-09-04

EARLIER PELLING DATE: 1998-03-06

EARLIER PELLING DATE: 1997-03-07

EARLIER PELLING DATE: 1997-05-03

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EARLIER PILING DATE: 1997-04-11
EARLIER APPLICATION WUMBER: 60/043,674
EARLIER PILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-02
EARLIER FILING DATE: 19

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Wed Sep

RESULT 8 US-08-250-958-3 ; Sequence 3, Application US/08250958 ; Patent No. 5571713

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61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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GENERAL INFORMATION:

APPLICANT: Lyle, Leon
APPLICANT: Thomas-Miller, Beth
TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
TITLE OF INVENTION: VASCULAR RESTENOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millinckrodt Medical, Inc.
STREET: 675 McDonnell Boulevard, P.O. Box 5840
                                                                                                                                                                                                                                                                                                                                                                                                                                   COURTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHALIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 13-JAN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Monocyte Chemotactic Protein-1 STRAIN: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/182,917
FILING DATE: 14-UAN-1994
APPLICATION NUMBER: US 07/965,678
FILING DATE: 22-CCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vacca, Rita D.
REGISTRATION NUMBER: 33,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION:
TELEPHONE: 314-895-7215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFACE 314 4895-2156
TELEFAX: 314 4895-2156
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 base pairs
TVOR: MUCLEIC acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: MRNA
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                                                                                                                                                                                                                                                                                               STREET: 675 McDo
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: lin
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PCT-US95-00605-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1289 GTGATCTTCAAGACCATGTGGCCAAGAGATCTGTGCTGACCCCAAGGAGAGGGTT 1348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAGCCAGATGCAATGACCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CAGGATICCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER APPLICATION NUMBER: 60/056,811
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,809
EARLIER PELING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER PELING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER PELING DATE: 1997-08-60/65
EARLIER FILING DATE: 1997-08-60/66
EARLIER 
                                                          EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-06-3
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Best Local Similarity
Matches 227; Conserva
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61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120 202 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT

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181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACT 219

Sequence 29, Application US/09463451; Patent No. 6537779
GENERAL INFORMATION: US-09-463-451-29

APPLICANT: KARA, Buhpendra V. PIOLI, David

CORRESPONDENCE ADDRESS:

ADDRESSE: Pillsbury Madison & Sutro, L.L.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STREET: 1000
CUNTRY: USA
ZIP: 20005-3918
COMPUTER: ENDOPY disk
COMPUTER: TOPPY disk
COMPUTER: TOPPY disk
COMPUTER: TOPPY SYSTEM:
MEDIUM TYPE: Floppy disk
COMPUTER: DAY Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US /09/463,451
FILING DATE: 03-Apr-2000
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION NUMBER: PCT/GB98/02175
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: REB 9715660.8
FILING DATE: 25-JUL-1997
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 base pairs

ö

DB 1; Length 228;

98.6%; Score 224.8; DB 1; 80.7%; Pred. No. 2.4e-60; tive 42; Mismatches 2;

Query Match Best Local Similarity 80.7 Matches 184; Conservative

, ANTI-SENSE: NO US-08-250-958-3

Indels

US-09-463-451-29

86.0%; Score 196; DB 4; Length 213; 97.5%; Pred. No. 1.9e-51; tive 0; Mismatches 5; Indels Query Match Best Local Similarity 97.55 Matches 199; Conservative 25 GTCACCTGCTGTTATAACTTCACCAATAGGAAGATCTCAGTGCAGAGGCTCGCGAGCTAT

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61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120 61 UCAGUGCAGAGGCUCGCGAGCUADAGAAUCACCAGCAGCAAGUGUCCCAAAGAAGAU 120 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180 1 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228 CAGGAUUCCAUGCACCACCUGGACAAGCAAACCCAAAGUCCGAAGACU 121 δ 원 δ g ð

RESULT 9
5212073-1
;Paten 10. 5212073
APPLICANT: ROLLINS, BARRETT;STILES, CHARLES;WONG, GORDON G.
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/351,008

SEQ ID NO:1: ; LENGTH: 752 5212073-1

GENERAL INFORMATION:
APPLICANT: LYLB, LEON R.
APPLICANT: WINKEL, STEVEN L.
APPLICANT: STRIETER, ROBERT M.
TITLE OF INVENTION: THERAPECUTIC TREATMENT FOR INHIBITING
TITLE OF INVENTION: TASCULAR RESTENOSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W

CITY: Washington STATE: D. C. COUNTRY: U.S.A.

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322 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACT 360

COUNTRY: U.S.A.

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,958
FILING DATE: 27-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/965,678
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALKER, Barbara W.
REGISTRATION NUMBER: 35,400
REPREBUCE/DOCKET NUMBER: 35,400
REPREBUCE/DOCKET NUMBER: 35,400
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATIOS:
TELECOMMUNICATION ON: 3:
SEQUENCE CHARACTERESTICS:
LENGTH: 228 base pairs
TYPE: nucleic acid
STANDEDINESS: single
TYPE: nucleic acid
STANDEDINESS: linear
MOLECULE TYPE: mRNA

BUNDELL, Kenneth R.
HOCKNEY, Robert C.
TITLE OF INVENTION: T' Promoter-Based Expression System
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

LENGTH: 213 base pairs TYPE: nucleic acid STRANDEDNESS: single

TOPOLOGY: linear MOLECULE TYPE: other nucleic acid SEQUENCE DESCRIPTION: SEQ ID NO: 29:

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Sequence 13, Application US/07927391

Batent No. 6001649

GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: MINCUX, Brigitte
APPLICANT: WITY, Adrian
APPLICANT: VITA, Natalio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: protein having a cytokin type
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGTGCTGACCCCAAGCAGAAGTGGGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 graarcricaagaccaaacrggacaaggarcrigrigrigaccccacacagaagrgggic 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
STREET: ROAD, PO BOX 299
STREET: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.0%; Score 148.2; DB 3; 78.7%; Pred. No. 1.1e-36; ive 0; Mismatches 48;
                             205 AAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19920929
CHASSIFICATION: 530
                                                      30 AAGCAAACCCAAACTCCGAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REPRENCK/POCKET NUMBER: 1678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
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Matches 177; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                             RESULT 12
US-07-927-391-13
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                                                                                                                                                                      AAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGATTCCATGGACCACCTGGAC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144
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84
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                                                                          AGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCTGTGATCTTCAAGACCATTGTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GTCACCTGCTGTTATAACTTCACCAATAGGAAGATCTCAGTGCAGAGGCTCGCGAGCTAT
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Patent No. 6537779
GENERAL INFORMATION:
APPLICANT: KARA, Buhpendra V.
PIOLI, David
BUNDELL, Kenneth R.
HOCKNEY, DOCKNEY, TO Promoter-Based Expression System NUMBER OF SEQUENCES: 32
CORRESPONDENCE BILISHULY Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.0%; Score 196; DB 4; Length 213; 97.5%; Pred. No. 1.9e-51; or Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER LOSA

ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/463,451
FILING DATE: 03-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: PCT/GB98/02175
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: GB 9715660.8
FILING DATE: 25-JUL-1998
APPLICATION NUMBER: GB 971560.8
FILING DATE: 25-JUL-1997
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                             205 AAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                       AAGCAAACCCAAACTCCGAAGACT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 213 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 97.5
Matches 199; Conservative
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FEATURE:
NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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; LOCATION:
US-07-927-391-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 CCTAAGCAGAGGCTGGAGAGCTACAGAAGGACCACCAGTAGCCACCAGCAGCACCAGCAGGAAGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGGAAGTGGGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 GTAATCTTCAAGACCAAACTGGACAAGGAGATCTGTGCTGACCCCACACAGAAGTGGGTC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60
                                                                                                                                                                                 Sequence 1273, Application US/09016434

Patent No. 650038
GENERAL INFORMATION
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTTE PHYRMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: USA
181 CAGGACTTTATGAAGCACCTGGACAAGAAAACCCAAACTCCAAAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 caddacirrardaadcaccredacaadaaacccaaacrecaaag 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.0%; Score 148.2; DB 4; Length Best Local Similarity 78.7%; Pred. No. 1.8e-36; Matches 177; Conservative 0; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPM COMPATIBLE
COMPUTER: DEC. FOOS/MS-DOS
SOFTWARE: WORD PErfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
RPPLICATION DATA:
FILING DATE: HEREWITH
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ATION NUMBER:
AGDATE: HEREWITH
SSIFICATION L.
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ASFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: Karen J.
ATTONEN'APADIT TON:
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RESULT 14

Sequence 15, Application US/07927391

Sequence 15, Application US/07927391

Patent No. 6001649

GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: MINTY, Adrian
APPLICANT: MINTY, Adrian
APPLICANT: WITA, Natalio
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: for its preparation.

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal 140 CAGCCAGTTGGGATTAATACTTCCAACTACCTGCTGCTACAGATTTATCAATAAGAAAATC 199 61 TCAGTGCAGAGGTTCGCGAGCTATAGAAGAATCACCAGCAAGTGTGCCGAAAGAAGTT 120 121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180 260 GTAATCTTCAAGACCAAACTGGACAAGGAGATCTGTGCTGACCCCACACAGAAGTGGGTC 319 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 200 CCTAAGCAGAGGCTGGAGAGGACTACAGAAGGACCACCAGTAGCACTGTCCCCGGGAAGCT . 0 Length 814; Indels STWALE,
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PROFESSION PC CONSTINCT
OFFRATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/927,391
**TITING DATE: 19920929 Query Match 65.0%; Score 148.2; DB 3; Best Local Similarity 78.7%; Pred. No. 1.8e-36; Matches 177; Conservative 0; Mismatches 48; 16781/369 APPLICALL...
FILING DATE: 1992092,
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 1678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TTELEPHONE: (703) 836-9300 LENGTH: 814 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single TELEFAX: (703) 683-410 TELEX: 899149 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: sig_peptide 41..367 CITY: ALEXANDRIA STATE: VIRGINIA COUNTRY: USA linea

```
PATENT NO. 90.0249;
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: FERRARA, Pascual
APPLICANT: MILOUX, Adrian
APPLICANT: MILOUX, Adrian
APPLICANT: MILOUX, Natalio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: For its preparation.
TITLE OF INVENTION: for its preparation.
CORRESPONDENCES: 25
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO BOX 299
CITY: ALEXANDERA
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Best Local Similarity 78.6%; Pred. No. 2.4e-36;
Matches 176; Conservative 0; Mismatches 48; Indels 0.
181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAG 225
                          320 CAGGACTITAIGAAGCACCTGGACAAGAAAACCCAAACTCCAAAG 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/927,391
FILING DATE: 19920929
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENY INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFRERNCE/DOCKET NUMBER: 16781/369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 22313-0299
COMPUTER READBALE FORM:
MEDIUM TYPE: FLODY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      Sequence 17, Application US/07927391
Patent No. 6001649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 899149

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
US-07-927-391-17
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Search completed: August 31, 2004, 02:59:28 Job time : 56 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                  - nucleic search, using sw model
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August 31, 2004, 02:59:34; Search time 254 Seconds (without alignments) 4417.658 Million cell updates/sec 07330446 228 1 cagccagatgcaatcaatgc.....aaacccaaactccgaagact 3237270 segs, 2460713050 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Published Applications NA:*

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2: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US08_DUBCOMB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/US08_DUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli	Sequence 209, App	Sequence 213, App	Sequence 3105, Ap	Sequence 72, Appl	Sequence 66, Appl	Sequence 1344, Ap	Seguence 58, Appl	Sequence 17, Appl	Sequence 849, App	Sequence 849, App	Sequence 396, App	Sequence 1165, Ap	Sequence 210, App
ΠD	US-10-276-971-3	US-10-449-831A-209	US-10-449-831A-213	US-10-060-036-3105	US-09-777-430A-72	US-10-210-120-66	US-10-641-643-1344	US-10-283-975A-58	US-10-764-649-17	US-10-342-887-849	US-10-172-118-849	US-10-170-385-396	US-10-641-643-1165	US-10-133-013-210
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% Query Match Length DB	228	294	405	475	647	725	725	725	725	739	739	739	741	756
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	228	228	228	228	228	228	228	228	228	228	228	228	228	228
Result No.	Н	2	m	Ω	ហ	9	7	a o	σν	10	11	12	13	14

Sequence 377, App Sequence 10, Appli Sequence 18, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 54, Appl Sequence 54, Appl Sequence 106, App Sequence 107, App Sequence 107, App Sequence 76, Appl Sequence 76, Appl Sequence 76, Appl Sequence 22639, A Sequence 22639, A Sequence 22639, A Sequence 211, App Sequence 211, App Sequence 113, App Sequence 1213, App Sequence 81, Appl Sequence 81, Appl Sequence 91, Appl
US-10-388-360-377 US-10-1339-778-1 US-10-1339-778-1 US-10-1339-778-1 US-10-134-090-583 US-09-792-793A-53 US-09-792-793A-53 US-09-792-793A-53 US-09-792-793A-54 US-10-375-209A-54 US-10-375-209A-53 US-09-792-793A-54 US-10-375-209A-54 US-09-981-876-106 US-09-981-876-109 US-10-040-739-739 US-10-041-090-839 US-10-305-720-1273 US-10-305-720-1273 US-10-305-720-1273 US-10-305-720-1273 US-10-044-090-837 US-10-717-597-95
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ALIGNMENTS

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US-LUCATORY APPLICATION US/10276971
; Sequence 3, Application US/10276971
; Publication No. US20030162737A1
; FABREAL INFORMATION:
; APPLICANT: Egashira Kensuke
; APPLICANT: Yoshiyaki Inada
; TILE REFERENCE: 2733 USP
; CURRENT APPLICATION NUMBER: US/10/276,971
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 228; DB 15; Length 22. Best Local Similarity 100.0%; Pred. No. 6.4e-66; Matches 228; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-10-276-971-3
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145 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTATAACTTCACCAATAGGAAGATC 204
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                                                                                                                                                                                                                                                                                                                                                                                                      404 CAGCCAGATGCAATGAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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Sequence 3105, Application US/10060036

Publication NO. USC030073144A1

Sequence 3105, Application US/10060036

Publication NO. USC030073144A1

APPLICANT: Benson, Darin R.

APPLICANT: Hodes, Michael D.

APPLICANT: Persing, David H.

APPLICANT: Hopler, William T.

APPLICANT: Hopler, William T.

APPLICANT: Hopler, William T.

APPLICANT: Hopler, William T.

APPLICANT: OS INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

ITILE OF INVENTION: AND DIAGNOSIS OF PANCERATIC CANCER

FILE REFERENCE: 210.121.566

CURRENT APPLICATION NUMBER: US/10/060,036

CURRENT FILING DATE: 2002-01-30
               Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 CAGGATTCCATGGACCACCTGGACAAGCAAACCCGAAGCT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT
                                                                        Indels
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100.0%; Score 228; DB 13;
100.0%; Pred. No. 8e-66;
. Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 228; DB 15; Best Local Similarity 100.0%; Pred. No. 8.6e-66; Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3105
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Query Match
100.0%; Score 228; DB 17;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: 934513
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1344
US-10-641-643-1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                            RESULT 7
US-10-641-643-1344
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APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Allawi, Hatim T.
APPLICANT: Wayland, Sarah R.
APPLICANT: Wayland, Sarah R.
APPLICANT: Takova, Tsetska
APPLICANT: Neir, Bruce P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REPRESENCE: FORS-04912
CURRENT APPLICATION NUMBER: US/09/777,430A
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
LENGTH: 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 CAGCCAGAUGCAAUCAAUGCCCCAGUCACCUGCUGUUAUAACUUCACCAAUAGGAAGAAC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGATTCCATGGACCACTGGACAAGCAAACCCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 CAGGAUUCCAUGGACCACCUGGACAAGCAAAACCCAAAACUCCGAAGACU 297
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 228; DB 9; Length 647;
Best Local Similarity 81.6%; Pred. No. 9.7e-66;
Matches 186; Conservative 42; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-210-120-66

Sequence 66, Application US/10210120

Publication No. US20030175736A1

GENERAL INFORMATION:
APPLICANT: Chinnaiyan, Arul M.
APPLICANT: Chinnaiyan, Arul M.
APPLICANT: Rubin, Mark Arun
TITLE OF INVENTION: Expression Profile of Prostate Cancer
TITLE OF INVENTION: Expression Profile of Prostate Cancer
FILE REFERENCE: UM-07221
CURRENT FILING DATE: 2002-08-01

PRIOR APPLICATION NUMBER: US 60/309,581

PRIOR PILING DATE: 2001-08-02

PRIOR PILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 123

SOFTWARE: Patentin Version 3.2

SEQ ID NO 66

LENGTH: 725
                                                                                                                                                                                                                                                                                         ; TYPE: RNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Synthetic
US-09-777-430A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Homo sapiens
US-10-210-120-66
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ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Competible
 ODEFWARE: Word Perfect 6.1 for Windows/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/641,643
 FILING DATE: 4-Aug-2003
 CLASSIFFCATION NUMBER: ADACHORY
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 97,071
 REGISTRATION ; 0 Sequence 1344, Application US/10641643

Sequence 1344, Application US/10041643

Publication No. US20040077003A1

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Sugan G. Stuart
Jeffrey J. Seilhamer
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD
GENE EXPRESSION Length 725; 303 caggarrccargeaccaccregacaagcaaacccaaacrccgaagacr 350 181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT Indels

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Best Local Similarity 100.
Matches 228; Conservative
                                                                                                              ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)...(353)
US-10-764-649-17
                                                                     TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ношо
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; ORGANISM: Homc
US-10-342-887-849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, Halyan
APPLICANT: Xu, Halyan
APPLICANT: Xu, Halyan
APPLICANT: Xu, Halyan
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Barnes, Olem
TITLE OF INVENTION: METADOLE DISORDERS
FILE REFERENCE: MP12003-025PIRNM
CURRENT APPLICATION NUMBER: US/10/764,649
PRIOR APPLICATION NUMBER: G0/446041
PRIOR APPLICATION NUMBER: 60/446041
NUMBER OF SEQ ID NOS: 20
  243 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGGAGGGGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 182
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                                                                                                                                                                                                                                       Sequence 56, Application US/10283975A
Sequence 56, Application US/10283975A
Publication No US20040110792A1
Sequence 56, Application.
Hubblication No US20040110792A1
Septicant No US20040110792A1
APPLICANT: Ortho-Clinical Diagnostics, Inc.
TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
FILE REFERENCE: COS 293 FOT STATE TELE REFERENCE: COS 293 FOT STATE APPLICATION NUMBER: US/10/283,975A
CURRENT FILING DATE: 2002-10-30
FRIOR FILING DATE: 2001-10-30
PRIOR FILING DATE: 2001-10-30
SEQ ID NOS: 900
SOFTWARE: PatentIn Version 3.1
ENGTH: 725
                                                                                      181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                               303 CAGGATTCCATGGACCACCTGGACAAGCCAAACTCCGAAGACT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 228; DB 17; Length 725; 100.0%; Pred. No. 1e-65; 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CRGANISM: HUMAN
US-10-283-975A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-764-649-17
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APPLICANT: Dai, Hongvue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Linsley, Peter S.
APPLICANT: Money Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer' Laura Johanna
APPLICANT: Van 't Veer' Laura Johanna
APPLICANT: Van 'd Veer' Laura Johanna
APPLICANT: Van 'd Veer' Laura Johanna
APPLICANT: Van 'd Veer' Laura Johanna
APPLICANT: Bernards, Rene
TILLE REFERENCE: 930-108-999
CURRENT PELLING DATE: 2003-09-918
PRIOR PAPLICATION NUMBER: 60/298,918
PRIOR PAPLICATION NUMBER: 60/298,918
PRIOR PAPLICATION NUMBER: 60/380,710
PRIOR PLING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
TENNORM: 730
TENNORM: 730
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                                                                                                                                                                                                                                                                                                        Length 725;
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                                                                                                                                                                                                                                                                                                        DB 17;
                                                                                                                                                                                                                                                                                                     100.0%; Score 228; D
100.0%; Pred. No. 1e-
ive 0; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17 LENGTH: 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 849, Application US/10342887; Publication No. US20040058340A1; GENERAL INFORMATION:
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243 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 302
                         243 GIGATCTICAAGACCATIGIGGCCCAAGGAGAICTGTGCTGACCCCAAGCAGAAGTGGGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCCAGATGCAATGAATGCCCCAGTCACCTGTTATAACTTCACCAATAGGAAGATC 60
                                                                                                                                                                                                                                             us-10-1/4-118-849;
gequence 849, Application US/10172118
publication No. US20030224374A1
genence 849, Application US/10172118
publication No. US20030224374A1
general INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mac
APPLICANT: Wan de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Wan de Vijver, Marc
CURRENT Bernards, Recessor (202-06-14
NUMBER OF SEQ ID NOS: 2699
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
TYPE: DNA
OKRANISM: Homo sapiens
PUBLICATION INPORMATION:
DATABASE ENTRY DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
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                                                                                                                          303 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 350
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                                                                                              181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 228; DB 13; Length 7 Best Local Similarity 100.0%; Pred. No. 1e-65; Matches 228; Conservative 0; Mismatches 0; Indels
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US-10-170-385-396
US-10-170-385-396
Sequence 396, Application US/10170385
Publication No. US20030203372A1
GENERAL INFORMATION:
APPLICANT: Ward, Neil Raymond
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: Harris, Robert Alan
APPLICANT: Binley, Katie Mary
APPLICANT: Raymor, William Nigel
APPLICANT: Raymor, William Nigel
APPLICANT: Raymor, Stuart
APPLICANT: Naylor, Stuart
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
                                                                                                                                                                                                                                           -10-172-118-849
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US-10-641-643-1165
Sequence 1165, Application US/10641643
; Sequence 1165, Application US/10641643
; Publication No. US20040077003A1
; Publication No. US20040077003A1
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeshinamer
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COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

SOFTWARE: WAR PELFOCE, 6.1 for Windows/MS-DOS

SOFTWARE: WAR PEFFECT, 6.1 for Windows/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: CUNROWN>

FILING DATE: CANADOWN>

FILING DATE: CANADOWN>

FILING DATE: CANADOWN>

FILING DATE: CANADOWN>

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

RESPERENCE DOCKET NUMBER: 37,071

REFERENCE DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 350
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ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 53268200100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR PILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSEQ for Windows Version 4.0
SSOTUMARE: 739
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CORGANISM: Homo Sapiens
US-10-170-385-396
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; ORGANISM: Homo sapiens
US-10-388-360-377
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US-10-13--013-210
Sequence 210, Application US/10133013
Subdication No. US20030166903A1
Subdication No. US20030166903A1
GENERAL INFORMATION:
APPLICANT: Bardomn, Olga
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
TITLE CF INFORMION: GENERS ASSOCIATED WITH VASCULAR DISEASE
FILE REFERENCE: PA-0049 US
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR FILING DATE: 2001-04-27
NUMBER OF EGO ID NOS: 271
SOFTWARE: PERL PROGram
SSOTURN OF SEQ ID NOS: 271
SOFTWARE: PERL PROGram
SSOTURN OF SEQ ID NOS: 271
SENGTH: 756
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100.0%; Score 228; DB 15; Length 'Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: Incyte ID No. US20030166903A1 470784CB1
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                      CLONE: 9187434
SEQUENCE DESCRIPTION: SEQ ID NO: 1165 :
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
                                                                                                   LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 377, Application US/10388360

Publication No. US2003022528A1

GENERAL INFORMATION:

APPLICANT: GENOMIC HEALTH

APPLICANT: Crohin, Maureen T.

APPLICANT: Shak, Steve

APPLICANT: Michael Graham

TILE REFERENCE: 39740-0001US

CURRENT FILING DATE: 2003-03-13

PRIOR PELICATION NUMBER: US/10/388,360

CURRENT FILING DATE: 2003-03-12

PRIOR PELICATION NUMBER: US 60/312,049

PRIOR PELICATION NUMBER: US 60/364,890

PRIOR FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 384

SOFTWARE: FREESE for Windows Version 4.0

SOFTWARE: FREESE FREESE for Windows Version 4.0
262 GIGATCTICAAGACCAITGIGGCCAAGGAGATCTGTGCTGACCCCAAGGAGAGTGGGTT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 CAGCCAGATGCAATCAATGCCCCAGTCACCTGTTATAACTTCACCAATAGGAAGATC 200
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                                                                                                    181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228
                                                                                                                                                            322 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 369
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Job time : 256 secs
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August 30, 2004, 16:49:12; Search time 1941 Seconds (without alignments) 4133.145 Million cell updates/sec
                                                                            07330446
228
1 cagccagatgcaatcaatgc.....aaacccaaactccgaagact 228
                                                                                                                                                                                                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                    37577330 seqs, 17593059518 residues
                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                               - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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length: 200000000
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Maximum DB seq
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Sequence:
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                                               Run on:
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44: | cgn2_6/ptodata/2/pna/US100B_COMB.seq: 44: | cgn2_6/ptodata/2/pna/US101A_COMB.seq: 44: | cgn2_6/ptodata/2/pna/US101A_COMB.seq: 44: | cgn2_6/ptodata/2/pna/US101B_COMB.seq: 44: | cgn2_6/ptodata/2/pna/US101B_COMB.seq: 45: | cgn2_6/ptodata/2/pna/US6001_COMB.seq: 45: | cgn2_6/ptodata/2/pna/US6001_COMB.seq: 45: | cgn2_6/ptodata/2/pna/US6001_COMB.seq: 46: | cgn2_6/ptodata/2/pna/US6002_COMB.seq: 46: | cgn2_6/ptodata/2/pna/US6003_COMB.seq: 46: | cgn2_6/ptodata/2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Gaps

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Indels

Length 228;

120 120

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Result

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CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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TITLE OF INVENTION: Higher molecular weight entities and uses therefor
FILE REFERENCE: 2385978
FULE REFERENCE: 2385978
CURRENT APPLICATION UNMBER: US/10/449,831A
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: USSN 60/384878
PRIOR APPLICATION NUMBER: USSN 60/384878
NUMBER OF SEQ ID NOS: 237
SOFTWARE: PATE: 1002-05-31
NUMBER OF SEQ ID NOS: 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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100.0%; Pred. No. 7.5e-58;
iive 0; Mismatches 0;
   Query Match 100.0%; Score 228; DB 48; Best Local Similarity 100.0%; Pred. No. 6.9e-58; Matches 228; Conservative 0; Mismatches 0;
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Les 228; Conservative
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; LOCATION: (1)..(294)
US-10-449-831A-209
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ORGANISM: Human
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LENGTH: 294
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Sequence 3, Application US/10276971

APPLICANT: Equality Solition

APPLICANT: Yashliro Iseda

APPLICANT: Yashliro Iseda

APPLICANT: Yoshlivki Inada

TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension

TITLE REFERENCE: 2733 USOR

CURRENT APPLICATION NUMBER: US/10/276,971

UNMBER OF SEQ ID NOS: 4

SEQ ID NOS: 4

SEQ ID NOS: 4

SEQ ID NOS: 4
                                                                                                                               Sequence 209, App Sequence 111, App Sequence 111, App Sequence 113, App Sequence 113, App Sequence 113, App Sequence 111, App Sequence 111, App Sequence 1124, App Sequence 1124, App Sequence 211, App Sequence 2118, App Sequence 2118, App Sequence 2118, App Sequence 1183, App Sequence 1196, App Sequence 1196, App Sequence 1376, App Sequence 1376, App Sequence 1376, App Sequence 1376, App Sequence 136, App Sequence 1361, App Seq
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8614, Ap
7825, Ap
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US-09-442-346A-1139

US-09-442-346A-1139

US-09-442-36A-1139

US-09-442-36A-1139

US-09-442-59B-37

US-09-534-843-79

US-09-534-843-796

US-09-726-791-1190

US-09-726-791-793

US-09-710-788-17783

US-09-534-843-7956

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US-09-710-788-788-783

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US-09-699-998-7825
Query
Match Length DB
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246 181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228 247 CAGGATTCCATGGACCACCTGGACAAGCAAAACCCAAACTCCGAAGACT 294 APPLICANT: Chenchik, Alex APPLICANT: Lukashev, Matvey TITLE OF INVENTION: Hematology/Immunology Array

TYPE: DNA ORGANISM: Human

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Length 294;

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181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Homo sapiens
US-09-221-481-519
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US-09-442-366A-1139
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100.0%; Score 228; DB 20; Length 348;
Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0
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GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey
ITILE OF INVENTION: Hematology/Immunology Array
FILE REFERENCE: CLON-006CIPLS
CURRENT APPLICATION WUMBER: US/09/442,384B
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 830
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 161
LENGTH: 348
    CURRENT APPLICATION NUMBER: US/09/442,384A
CURRENT FILING DATE: 1999-11-17
PRIOR PILING DATE: 1998-03.31
NUMBER: 05 DI NOS: 830
SOFTWARE: 1854ESQ for Windows Version 4.0
SEQ ID NO 161
LENGTH: 348
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, OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384B-161
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ORGANISM: Artificial Sequence
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US-09-442-384B-161
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284 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 331
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Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 228; DB 16; Best Local Similarity 100.0%; Pred. No. 7.9e-58; Matches 228; Conservative 0; Mismatches 0;
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APPLICANT: Chenchik, Alex APPLICANT: Chenchik, Alex APPLICANT: Chenchik, Matvey E. TITLE OP INVENTION: Human Array FILE REFERENCE: CLON-006CIP13 CURRENT APPLICATION NUMBER: US/09/442,366A CURRENT FILING DATE: 1999-11-17 PRIOR FILING DATE: 1999-11-17 PRIOR FILING DATE: 1998-03-31 NUMBER: OF SEQ ID NOS: 2216 SEQ ID NO 1139 CESTION NUMBER: APPLICATION NUMBER: OF SEQ ID NO 1139 CESTION NUMBER: OF SEQ ID NO 1139 CESTION NUMBER: APPLICATION NUMBER: OF SEQ ID NO 1139 CESTION NUMBER: APPLICATION NUMBER: OF SEQ ID NO 1139 CESTION NUMBER: APPLICATION NUMBER: OF SEQ ID NO 1139 CESTION NUMBER: APPLICATION NUMBER: OF SEQ ID NO 1139 CESTION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: OF SEQ ID NO 1139
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Sequence 519, Application US/09221481
SEQUENCE 519, Application US/09221481
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Chenchik, Alex
TITLE OF INVENTION: Human Array
FILE REFERENCE: CLON-006CIP6
CURRENT APPLICATION NUMBER: US/09/221,481
CURRENT FILING DATE: 1998-12-28
PRIOR FILING DATE: 1998-12-28
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 589
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 519
LENGTH: 349
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US-09-442-589B-37
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        SEQ ID NO 37
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CAGCCAGATGCAATCAATGCCCCAGTCACTGTTATAACTTCACCAATAGGAAGATC 163
                                                          TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
                                                                                      TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 223
                                                                                                                                     GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT 180
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100.0%; Pred. No. 7.9e-58;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LUKESHEW, MATURY, TITLE OF INVENTION: Hematology/Immunology Array, FILE BEFERENCE: CLON-006CTP15
CURRENT APPLICATION NUMBER: US/09/442,384
CURRENT APPLICATION NUMBER: 09/053,375
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 415
SCFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 161
LENGTH: 349
TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: Lukashev, Matvey
TITLE OF INVENTION: Human Cardicvascular Array
FILE REPERENCE: CLON-006CIP10
CURRENT APPLICATION NUMBER: 105/04/42,589A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 597
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384-161
                                                                                                                                                                                                                                                                                                                                             ; Sequence 161, Application US/09442384; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 228; Conservative
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US-09-442-384-161
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US-09-442-589A-37
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APPLICANT: Chencilk, Matvey
ITLE OF UNVENTION: Human Cardiovascular Array
ITLE OF UNVENTION: Human Cardiovascular Array
FILE REFERENCE: CLON-006CIPL0
CURRENT APPLICATION NUMBER: US/09/442,589B
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 1194
SEQ ID NO 37
LENGTH: 349
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                                                     FEATURE:

COTHER INFORMATION: nucleic acid probe US-09-442-589A-37
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Matches 228; Conservative 0;
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Simi
Matches 228;
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         CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
                                                                                                                     TCAGTGCAGAGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
                                                                                                                                                                         GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCCTGACCCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koenegen, Frank
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
CURRENT APPLICATION NUMBER: US/10/449,831A
CURRENT FILING DATE: 2003-05-30
PRIOR PILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 237
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: Patentin Version 3.2
LENGTH: 405
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US-09-287-618-16749
; Sequence 16749, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.;
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED;
; TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-768
; CURRENT APPLICATION NUMBER: US/09/287,618
; CURRENT FILING DATE: 1999-04-02;
; NUMBER OF SEQ ID NOS: 35865
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                 181 CAGGALTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT
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100.0%; Pred. No. 8.3e-58;
ive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 228; Conservative
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; LOCATION: (1)..(399)
US-10-449-831A-213
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US-10-449-831A-213
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Sellhamer, Angelo M.
APPLICANT: Stude, Laura L.
APPLICANT: Stude, Laura L.
APPLICANT: Wullahy, Sara J.
APPLICANT: Mughton, Rebecca E.
TITLE OF INVENTION: POLYNUCIBOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLEC
TITLE OF INVENTION NUMBER: US/09/534,843
CURRENT FILING DARE: 2000-03-24
CURRENT FILING DARE: 2000-03-24
NUMBER OF SEQ ID NOS: 49783
SOTWARE: PERL Program
SEQ ID NO 7971
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; GENERAL INPORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED;
TITLE OF INVENTION: NEOW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-768
CURRENT APPLICATION NUMBER: US/09/287,618
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 35865
SOFTHARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu01345546
US-09-534-843-7971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature; LOCATION: (1)...(403)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.
Matches 228; Conservative
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US-09-287-618-15642
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                                                                                                                     Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2009-001
CURRENT APPLICATION NUMBER: US/09/726,791
CURRENT FILING DATE: 2000-11-30
PRIOR PRIOR APPLICATION NUMBER: 60/168,127
PRIOR PRIOR APPLICATION NUMBER: 60/168,127
PRIOR PRIOR SEQ ID NOS: 1870
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 973
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                                                                                                                                                           Indels
                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 8.4e-58; Matches 228; Conservative 0; Mismatches 0;
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NAME/KEY: misc feature

LOCATION: (1)...(437)

OTHER INFORMATION: n = A,T,C or G
US-09-726-791-973
                  ; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-287-618-16749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
; SEQ ID NO 16749
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US-09-726-791-973
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Angelo M.
APPLICANT: Seilhamer, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Mullahy, Sara J.
APPLICANT: Maughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLECT CURRENT PAPLICATION NUMBER: US/09/534,843
CURRENT FILING DATE: 2000-03-24
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 49783
SOFTWARE: PERL Program
SEQ ID NO 1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu01000080
US-09-534-843-7953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: August 31, 2004, 04:19:46
Job time : 1944 secs
Application US/09534843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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5.1.6	Compugen
version	- 2004
Core	1993
Ger	ΰ
	Copyright

Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: August 30, 2004, 16:49:12 ; Search time 1465 Seconds (without alignments) 4647.493 Million cell updates/sec	Title: 07330446 Perfect score: 228 Sequence: 1 cagccagatgcaatcaatgcaaacccaaactccgaagact 228	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

27513289 segs, 14931090276 residues

Searched:

55026578

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST:*

1: em estba:*
2: em_esthum:*
3: em_esthum:*
5: em_esthum:*
6: em_esthum:*
6: em_esthum:*
7: em_estpl:*
10: gb_est2:*
112: gb_est2:*
113: gb_est3:*
114: gb_est2:*
115: em_esthum:*
116: em_esthum:*
117: em_gss_hum:*
118: em_gss_hum:*
119: em_gss_hum:*
120: em_gss_hum:*
121: em_gss_hum:*
122: em_gss_hum:*
133: em_gss_hum:*
144: gb_est5:*
155: em_gss_hum:*
165: em_gss_hum:*
176: em_gss_hum:*
177: em_gss_hum:*
187: em_gs Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AV661469 AV661469 AA047099 2k74a08.r AV714555 AV714555 BX490080 DKFZp686B
ΩΙ	432 9 AV661469 497 9 AA047099 513 9 AV714555 549 13 BX490080
8	9999
Query Match Length DB	432 497 513 549
Query Match Le	1000.00 1000.00 1000.00
Score	8888 5558 5558
Result No.	H 00 m 4

BM704915 UI-E-CII-	TAC CE	1442	9						BQ573817 UI-H-EZ0-											Č		9	8 AGENCOUR	CD522423 AGENCOURT	AV7	ω	CA307389 UI-H-FT1-	w.		BU199251 DCBCLG05	3393	œ	521 A	24954	2217	2574	٠ ص	1003 AGE	C)
12 BM70	12 EM70861	12 BM88823	9 AT.697816	10 AW77209	13 BU7309	13 BQ63116	12 BM9734	13 BU68536	13	14 CD6388	14 CB2679	Н	9 AV66113	14 CD6864	14	14	10	14	14	14	14	14 CD64118	14 CD64005	٦	σ	12	14 CA30738	14	σ	13 BU19925	14 CA44839	14	σ	13 BQ22495	13 BU1922	14 CD52257	13 BQ4326	13 BU6010	7
100	0.001	0.00		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0 73	100.0	100.0 74	100.0 74	100.0 75	100.0 75	100.0 76	100.0 76	100.0 78	100.0 78	100.0 79	100.0 82	100.0 85
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ALIGNMENTS

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AV714555 DCB Homo sapiens cDNA clone DCBADG05 5', mRNA sequence. AV714555 LB (I:10796072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

I bases 1 to 513.

Xu, X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Homo sapiens cDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
315 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                        /mol_type="mRNA"
/db_xref="CDB:3803121"
/db_xref="CDB:3803121"
/clone="INMAGE:488534"
/sex="female"
                                                                     organism="Homo sapiens"
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      High quality sequence stop: 487.
                           Location/Qualifiers
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Best Local Similarity 100.
Matches 228; Conservative
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SOURCE
ORGANISM
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JOURNAL
COMMENT
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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AV714555
                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 CAGCCAGATGCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC 175
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I (Dases 1 to 497)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoes,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hankins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Trevaskis,E., Schellenberg,K., Scares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R., and Marra,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                              /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/dev_bost="SOUR"
/lab_host="SOUR"
/clone_lib="GLC"
/note="Vector: pBluescript sk(-); Site_1: BcoRI; Site_2:
KhoT:
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Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 741 Std Error: 0.00
Seg primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAGCAGGAAGTGCCGAAGAAGT
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                            Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
Fax: 86-21-50801922
Email: hanzgechgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 228; DB 9;
100.0%; Pred. No. 1.1e-52;
iive 0; Mismatches 0;
                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCGSG05"
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                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 228; Conservative
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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AA047099
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                                                                FEATURES
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BX490080

DKFZD688B1371_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZD686B1371_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Emissions wiemann@dkfz- heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the oDNA
sequencing consortium of the German Genome Project. No s1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                 134 CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
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( Dases 1 to 549)

Ottenvaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Pobo, G., Han, M. and Wiemann, S.

EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/mol_type="mRNA"
/b xref="texton:9606"
/clone="DKFZp686B1371"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH10B"
/clone=libe="deso (synonym: hlcc3)"
/note="Vector: ptriplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
                                                                  /call_rype="dendritic cells"
/dev_stage="mature"
/lab_host="mature"
/lab_host="muss.g"
/note=luce lib=luce
/note="Vector: pTriplEx2; Site_l: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone (DKRZp686B1371) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                1 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAGGAGTGTCCCAAAGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGATTCCATGGACCACCTGGACAAGCAAACTCCGAAGACT
                                                                                                                                                                                                                                              100.0%; Score 228; DB 9; Length 5
100.0%; Pred. No. 1.2e-52;
'mol_type="mRNA"
'db_xref="taxon:9606"
'clone="DCBADG05"
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Homo sapiens
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                 228;
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1...563
| organism="Homo sapiens" |
| wol_type="mRNA" |
| wol_type="mRNA" |
| wol_type="mRNA" |
| wol_type="mRNA" |
| clone="UI="CII-agf"+04-0-UI" |
| tissue_type="mRPE and Choroid" |
| tissue_type="mRPE and Choroid" |
| tolone="UI="DHOB (Life Technologies) (TI phage resistant) |
| clone="Lib="UI="CII" |
| tissue_type="mred" |
| clone="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; ule-ECII is a normalized obna library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BM704915
UL-E-CII-agf-h-04-0-UI.rl UI-E-CII Homo sapiens cDNA clone
UI-E-CII-agf-h-04-0-UI.5', mRNA sequence.
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Email: bento-soares@uiowa.edu
Frasue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seg primer: M13 Reverse.
                                                                                                                                                   197
                                                                                                                                                                                                                                                       257
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bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 563)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                              CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                    TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
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                                                                                                   1 CAGCCAGATGCCAATGCCCCAGTCACCTGTTATAACTTCACCAATAGGAAGATC
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     Length 549;
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                                                   Indels
Query Match 100.0%; Score 228; DB 13; Best Local Similarity 100.0%; Pred. No. 1.2e-52; Matches 228; Conservative 0; Mismatches 0;
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Contact: Scares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9566
Fax: 319 335 9566
Email: bento-scares@uicwa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Scares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Scares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: M13 Reverse.
adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI).
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGTGCAGAGGTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
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                                                                                                                                                                                                                                                                                                                   Gaps
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UI-E-CI1-afw-i-08-0-UI.rl UI-E-CI1 Homo sapiens cDNA clone
UI-E-CI1-afw-i-08-0-UI 5', mRNA sequence.
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0
                                                                                                                                                                                                                                                                  Length 563;
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100.0%; Pred. No. 1.3e-52;
ive 0; Mismatches 0;
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/db xref="taxon:9606"
/clone="UI-B-CII-afw-i-08-0-UI"
/tissue_type="RPE and Choroid"
/dev_tage="adult"
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Matches 228; Conservative
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/clone_lib="UI-B-CII"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_lib="Enbray" containing the modified polylinker; Site_lib="Enbray" containing the UI-B-CII is a normalized cDNA library containing the following tissue(a): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM888255 59-002 S93 bp mRNA linear BST 08-MAR-2002 IMM174 Human Trabecular Meshwork cDNA library Homo sapiens cDNA 5',
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1 (bases 1 to 593)
Wirtz, M.K., Samples, J.R., Xu, H., Severson, T. and Acott, T.S.
Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-4698
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|mol_type="mRNA"
|db_xref="taxon:s606"
|tissue_type="eye"
|cell_type="trabecular meshwork"
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Email: wirtzm@ohsu.edu
Seg primer: T7 Reverse.
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A LOGACH AND STAIN, Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wyle,T., Martin,J., Blistain,A., Schmitt,A., Thekising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium
Unpublished (2000)
Cottact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ631442 117604.yl HR85 islet Homo sapiens cDNa clone IMAGE:6030414 5' similar to SW:SY02_HUMAN P13500 SWALL INDUCIBLE CYTOKINE A2 PRECURSOR ;, mRNa sequence.
             /clone_lib="Human Trabecular Meshwork cDNA library"
/note="Vector: pcDNA3; Site 1: EcoRI; Site 2: EcoRI; Human
cdNA library made from mRNA isolated from Erabecular
meshwork calls established fom eyes from 6 individuals,
ages 2 weeks to 2 years. Cells were harvested at passages
3 through 6. Invitrogen made a unidirectional cDNA library
from the mRNA from the frozen cells using a pcDNA3 vector
and TPO10F'' host cells."
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Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                      CAGCCAGATGCCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 594)
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Pred. No. 1.3e-52;
; Mismatches 0; Indels 0;
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Location/Qualifiers
host="TOP10F'"
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100.0%; Pre
tive 0; N
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Homo sapiens
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/mol_type="mRNA"

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AL697816 616 bp mRNA linear EST 04-SEP-2003
DXF22686E804104 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DXF22668E804104 5', mRNA sequence.
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg'de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
/lab.host="DH10B"
/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Nho1; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
Size-selected on agarose gel. Average insert size ~1kb. 5'
Amplified on agarose gel. Average insert size ~1kb. Maplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel:
114-362-1916, Fax: 314-747-2692."
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1 (bases 1 to 616)
Cytemwaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone (DKFZp686E04104) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 TCAGTGCAGAGGTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
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/db_xref="taxon:9606"
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Unpublished (2001)
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/clone="IMAGE:6030414" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" φ

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Matches 228;
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_nost="DHIOB"
/clone lib="NCI CGAP Kid11"
/clone lib="NCI CGAP Kid11"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs.
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NCI-CAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfilA, Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
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100.0%; Score 228; DB 9; Length 616;
Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:3032942"
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AW772091.1 GI:7704153
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University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
761: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
The following repetitive elements were found in this cDNA
sequence: 1-39, AAT.rich#Low_complexity (matched compliment)
Seg primer: M13 FORWARD
POLYA=Yes.
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                        603 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAAACTTCACCAATAGGAAGATC
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(cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Genome Res. 6 (9), 791-806 (1996)
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/organism="Homo sapiens"
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modified polylinker; Site_1: ECOR I; Site_2: Not I; UT-E-CII is a normalized CDMA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDMA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDMA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pTTMT-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDMA contains a library tag sequence that is located between the Not I site and the (dT)B tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG_TISSUE=RPE and Choroid TAG_LIB=UI-E-CI1 TAG_SEQ=ACCTA"

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                                                                  1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60
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634 bp mRNA linear EST 02-JUL-2002 ill7e04.xl HRB5 islet Homo sapiens cDNA clone IMAGE:6030414 3' similar to SW:SY02_HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2 PRECURSOR;, mRNA sequence. Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. BQ631169.1 GI:21682687 BQ631169 RESULT 12 BQ631169/c LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE

TITLE JOURNAL COMMENT

Endocrine Pañcreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Lahiller, L., Marran, M., Page, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Milliams, T., Jackson, Y. and Bowers, Y. Bendocrine Pancreas Consortium
Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Tel: 617-495-1812 Fax: 617-495-8557 MA 02138

/USB TITES THE NOTE OF THE NOTE; SIZE—SELECTED OF THE NOTE; SIZE—SELECTED OF THE NOTE; SIZE—SELECTED OF THE NOTE O obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -400P from Gibco
High quality sequence stop: 439.
Location/Qualifiers /organism="Homo sapiens" . .634 FEATURES

ORIGIN

Query Match

Length 634;

ö 180 61 TCAGTGCAGAGGCTCGGGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120 487 ergarcticaagaccarreregecaaggagarcrereregecegaecaggaagreerif 428 09 121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 1 CAGCCAGATGCAATGAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC Gaps ; 0 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 380 181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228 Indels 100.0%; Score 228; DB 13; Similarity 100.0%; Pred. No. 1.3e-52; 88; Conservative 0; Mismatches 0; Local Simi hes 228; 427 Matches 셤 ò 셤 ò g $\overset{\circ}{\circ}$ Dp

BM973445/c RESULT 13

BM973445 UI-CF-EC1-abx-n-09-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone UI-CF-EC1-abx-n-09-0-UI 3', mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 640) Bonaldo, M.F., Lennon, G. and Soares, M.B. BM973445.1 GI:19591036 Homo sapiens (human) Homo sapiens KEYWORDS SOURCE ORGANISM LOCUS ACCESSION VERSION

Genome Res. 6 (9), 791-806 (1996) discovery 97044477 MEDLINE PUBMED COMMENT REFERENCE AUTHORS TITLE JOURNAL

McCray Lab

Contact: McCray, PB

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//dev_stage="hung"
//dev_stage="hung"
//dev_stage="hung"
//dev_stage="hung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
//note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
//ICF-EC1 is a normalized cDNA library containing the following tisus(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digsered with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
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UI-CF-DU1-aav-j-23-0-UI.S2 UI-CF-DU1 Homo sapiens cDNA clone
UI-CF-DU1-aav-j-23-0-UI 3', mRNA sequence.
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).

The following repetitive elements were found in this cDNA Seq primer: M13 PORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          559 rcherechendencendenarian de la rechereche de la recherence de la reche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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TAG_SEQ=AAGTGCTTAC"
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Email: paul-mccrayeulowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.negen.com) or from Open Biosystems

(www.openbiosystems.com).

The following repetitive elements were found in this cDNA

Seq primer: Mi3 FORWARD

POLYA=Yes.
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1 (bases 1 to 640)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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TAG_LIB=UI-CF-DUI
TAG_SEQ=GGCTGTAGGC"
                                                                                                                                                                                      University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
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Best Local Similarity 100.0%; Pred. No. 1.3e-52;
Matches 228; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                    Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                        Contact: McCray, PB
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                                                                                                                                                                             McCray Lab
                                                                                                         97044477
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Search completed: August 31, 2004, 03:47:21
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/note="Gragan: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
/note="Gragan: Left Pelvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Orthospedics conthospedics controlled by Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soaresculowa.edu The following repetitive elements were found in this CDNA sequence: 1-39, AT rich#Low_complexity (matched compliment) POLYA=Yes.
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                                                                                        BOS73817 644 bp mRNA linear EST 19-JUN-2002 UI-H-EZO-bax-c-19-0-UI.sl NCI_CGAP_Chl Homo sapiens cDNA clone UI-H-EZO-bax-c-19-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
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1 (bases 1 to 644)
NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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